

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 13, 2003, 19:51:27 ; Search time 60 Seconds
(without alignments)
1099.318 Million cell updates/sec

Title: US-09-848-806-1

Perfect score: 2593

Sequence: 1 METKPNRRPNTVLPYQTP.....KLNLFNIADAFGVGKSD 495

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_101002.*

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- 22: /SID32/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 23: /SID32/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2593	100.0	495	AA048000	Arabidopsis CDPK2
2	2458	94.8	501	AA035776	Arabidopsis thalia
3	2458	94.8	501	AA048001	Arabidopsis CDPK4
4	2064	79.6	425	AA035777	Arabidopsis thalia
5	1932	74.5	512	AA093256	Soybean CDPK prote
6	1924	74.2	399	AA035778	Arabidopsis thalia
7	1742	67.2	483	AA031158	Arabidopsis thalia
8	1742	67.2	556	AA031157	Arabidopsis thalia
9	1703	65.7	856	AA038599	Arabidopsis thalia
10	1703	65.7	893	AA038598	Arabidopsis thalia

11	1703	65.7	1017	21	AA038597	Arabidopsis thalia
12	1509.5	58.2	549	23	AA052842	Physcomitrella pat
13	1509	58.2	408	21	AA031159	Arabidopsis thalia
14	1501	57.9	463	21	AA046565	Arabidopsis thalia
15	1500	57.8	280	22	AA065758	ATCDPK2 kinase dom
16	1462	56.4	529	21	AA029590	Arabidopsis thalia
17	1462	56.4	542	21	AA029589	Arabidopsis thalia
18	1460.5	56.3	459	21	AA029591	Arabidopsis thalia
19	1457	56.2	569	15	AA056237	Protein kinase spe
20	1325.5	51.1	538	21	AA043621	Arabidopsis thalia
21	1319	50.9	404	21	AA046566	Arabidopsis thalia
22	1231	47.5	378	21	AA046567	Arabidopsis thalia
23	1187.5	45.8	307	20	AA093255	Tobacco CDPK prote
24	1166.5	45.0	424	21	AA043622	Arabidopsis thalia
25	1153.5	44.5	421	21	AA043623	Arabidopsis thalia
26	1059	40.8	413	22	AA065755	ATCDPK kinase doma
27	1015.5	39.2	523	21	AA010101	Arabidopsis thalia
28	928.5	35.8	426	21	AA010102	Arabidopsis thalia
29	920.5	35.5	302	21	AA054428	Zea mays protein f
30	900	34.7	274	22	AA065756	ATCDPK1 kinase dom
31	887	34.2	274	19	AA049837	Amino acid sequenc
32	887	34.2	274	22	AA065757	ATCDPK1a Kinase do
33	887	34.2	274	22	AA065759	ATCDPK1a PK domain
34	849	32.7	597	23	AA052841	Physcomitrella pat
35	842.5	32.5	364	21	AA010103	Arabidopsis thalia
36	829	32.0	623	22	AA085583	Rice CDPK (clone r
37	771.5	29.8	456	16	AA074996	E. maxima Em70-1 a
38	753.5	29.1	504	21	AA016593	Arabidopsis thalia
39	753.5	29.1	594	21	AA016592	Arabidopsis thalia
40	737	28.4	502	21	AA053884	Arabidopsis thalia
41	737	28.4	594	21	AA053883	Arabidopsis thalia
42	712.5	27.5	428	21	AA016594	Arabidopsis thalia
43	712.5	27.5	524	21	AA018394	Plasmodium falcipa
44	694.5	26.8	189	23	AB059978	Human DITP polype
45	690.5	26.6	414	21	AA053885	Arabidopsis thalia

ALIGNMENTS

RESULT 1
AA048000
ID AA048000 standard; Protein; 495 AA.

AC AA048000;

XX 08-MAR-2002 (first entry)

XX Arabidopsis CDPK2 SEQ ID NO 1.

DE Arabidopsis CDPK2; CDPK4; calcium dependent protein kinase; oilseed;
KW disease resistance; agricultural; pathogen; crop yield; ornamental;
KW fungicide; bactericide; nematocide; insecticide; viricide; cereal;
KW transgenic; plant; enzyme.

OS Arabidopsis thaliana.

XX WO200184911-A1.

XX 15-NOV-2001.

XX 04-MAY-2001; 2001WO-US14368.

XX 05-MAY-2000; 2000US-201925P.

XX (GEO) GEN HOSPITAL CORP.

XX Sheen J;

XX WPI; 2002-062179/08.

XX N-PSDB; ABA06021.

XX Producing plant having increased disease resistance, comprises

PT

PT regenerating plant from a non-naturally occurring plant cell
PT over-expressing a polynucleotide encoding a calcium dependent protein
PT kinase polypeptide -
XX
XX
XX Disclosure; Fig 1; 44pp; English.
XX
CC The invention relates to producing a plant having increased disease
CC resistance, comprising providing a non-naturally occurring plant cell
CC expressing a polynucleotide encoding a calcium dependent protein
CC kinase (CDPK) polypeptide and regenerating a plant from the plant
CC cell, where the CDPK polypeptide is expressed in the plant, increasing
CC the resistance of the plant to disease as compared to a
CC naturally-occurring plant. The method is useful for a variety of
CC agricultural and commercial purposes including improving a plant's
CC resistance against plant pathogens, increasing crop yields, improving
CC crop and ornamental quality and reducing agricultural production costs.
CC The method facilitates an effective and economical method for in-plant
CC protection against plant pathogen, reducing or minimising the need for
CC traditional chemical practices (e.g. application of fungicides,
CC bactericides, nematocides, insecticides, or vorticides) that are typically
CC used by farmers for controlling the spread of plant pathogens and
CC providing protection against disease causing pathogens. The method
CC contributes to the production of high quality and high yield agricultural
CC products, e.g. fruits, ornamentals, vegetables, cereals and field crops
CC having reduced spots, blemishes and blotches that are caused by
CC pathogens, agricultural products with increased shelf-life and reduced
CC handling costs and high quality and yield crops for agricultural
CC (e.g. cereal and field crops), industrial (e.g. oilseeds) and commercial
CC (e.g. fiber crops) purposes. The present sequence is that of Arabidopsis
CC thaliana CDPK2 of the invention.
XX

Sequence	495 AA;
Query Match	100.0%; Score 2593; DB 23; Length 495;
Best Local Similarity	100.0%; Pred. No. 2e-222;
Matches	495; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 METKNPRPNTVLPYQTPRLRHYLLGKLGQGGTGYLCTEKSANYACKSIPKR 60
DB	1 METKNPRPNTVLPYQTPRLRHYLLGKLGQGGTGYLCTEKSANYACKSIPKR 60
QY	61 KLVCRDVEDVWREIQIMHLSHENPVRIKGTVEDSVFVHVMVECGGELFDRIVSKG 120
DB	61 KLVCRDVEDVWREIQIMHLSHENPVRIKGTVEDSVFVHVMVECGGELFDRIVSKG 120
QY	121 HFSREAVKLIKTILGWVEACHSLGWHRDLKPNFLFDSPKDDAKLKATDFGLSVFYKP 180
DB	121 HFSREAVKLIKTILGWVEACHSLGWHRDLKPNFLFDSPKDDAKLKATDFGLSVFYKP 180
QY	181 GOYLVDVGSPPYVAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFRQILQ 240
DB	181 GOYLVDVGSPPYVAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFRQILQ 240
QY	241 GKLDKSDPWTISEAAKDLIYKMLERSPKKISAEALCHPWIVDEQAAPDKPLDPAVL 300
DB	241 GKLDKSDPWTISEAAKDLIYKMLERSPKKISAEALCHPWIVDEQAAPDKPLDPAVL 300
QY	301 SRLKQSQWNKIKKMLRVAERLSEEBEGG-KELFKMTDNTNSGTTIFEELKAGLRKVG 360
DB	301 SRLKQSQWNKIKKMLRVAERLSEEBEGG-KELFKMTDNTNSGTTIFEELKAGLRKVG 360
QY	361 SELWSEIKSLMDAADIINSNGTIDYGEFLAATLHMNKWEREELVAAFSDFDKDGSGYIT 420
DB	361 SELWSEIKSLMDAADIINSNGTIDYGEFLAATLHMNKWEREELVAAFSDFDKDGSGYIT 420
QY	421 IDELQSACTEFGICDTPFLDMIKEDLDNDGKIDFSEFTAMWKRGGVGRSRTMMKNLNF 480
DB	421 IDELQSACTEFGICDTPFLDMIKEDLDNDGKIDFSEFTAMWKRGGVGRSRTMMKNLNF 480
QY	481 NIADAFGVGDKSDD 495
DB	481 NIADAFGVGDKSDD 495

RESULT 2	
AAG35776	
ID	AAG35776 standard; Protein; 501 AA.
XX	
XX	AAG35776;
XX	
XX	18-OCT-2000 (first entry)
DT	
XX	Arabidopsis thaliana protein fragment SEQ ID NO: 43753.
DE	
XX	Protein identification; signal transduction pathway; metabolic pathway;
KW	hybridisation assay; Genetic mapping; gene expression control; promoter;
KW	termination sequence.
XX	
OS	Arabidopsis thaliana.
PN	
XX	EP1033405-A2.
XX	
PD	06-SEP-2000.
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PF	25-FEB-2000; 2000EP-0301439.
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PR	03-MAR-1999; 99US-0123180.
PR	03-MAR-1999; 99US-0123548.
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PR 28-OCT-1999; 99US-0161361.
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PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 94.8%; Score 2458; DB 21; Length 501;
Best Local Similarity 94.8%; Pred. No. 2.2e-210;
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Db 3 KPNRRPSNSVLPYETPRLRDHYLLGKLGQGGQGTYYLCTEKSSSANYACKSIKPKLV 62
Qy 64 CREDYEDVWREIQIMHLSHPNVVIRKCTYEDSVFVHVWNEVCEGGELFDRIVSKGHS 123
Db 63 CREDYEDVWREIQIMHLSHPNVVIRKCTYEDSVFVHVWNEVCEGGELFDRIVSKGCF 122
Qy 124 EREAUKLIKILGWACHSLGWHRDLKPNFLFDPSPKDDAKLKATDFGLSVFYKPGQY 183
Db 123 EREAUKLIKILGWACHSLGWHRDLKPNFLFDPSPDDAKLKATDFGLSVFYKPGQY 182

QY 184 LYDVVGSPPYVAPVVKCCYCPEDVMSAGVILYLLSGVPEPWAETSGIFRQILQGLK 243
 DB 183 LYDVVGSPPYVAPVVKCCYCPEDVMSAGVILYLLSGVPEPWAETSGIFRQILQGLK 242
 QY 244 DFKSDPWPPTISEAAKDLIYKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAVLSRL 303
 DB 243 DFKSDPWPPTISEGAKDLIYKMLDRSPKKRISAHEALCHPWIVDEHAAPDKPLDPAVLSRL 302
 QY 304 KQFSQMKIKQWALRVIAERLSEEEIGLKLFPKIDTNSGTTITEELKAGLKRYSSEL 363
 DB 303 KQFSQMKIKQWALRVIAERLSEEEIGLKLFPKIDTNSGTTITEELKAGLKRYSSEL 362
 QY 364 MESEIKSLMDAADINSGTIDYGEFLAATLHMKNVREELVAFSDFDKDGSGYITIDE 423
 DB 363 MESEIKSLMDAADINSGTIDYGEFLAATLHMKNVREELVAFSDFDKDGSGYITIDE 422
 QY 424 LOSACTEFGLCDTPLDDMIKEIDLNDGKIDFSEFTAMMKKGDGVGRSRTMRNNLNFNIA 483
 DB 423 LOQACTEFGLCDTPLDDMIKEIDLNDGKIDFSEFTAMMKKGDGVGRSRTMRNNLNFNIA 482
 QY 484 DAFGVDG----EKSD 495
 DB 483 EAFGVEDTSSAKSD 498

RESULT 3
 ID AAM48001 standard; Protein; 501 AA.
 AC AAM48001;
 XX 08-MAR-2002 (first entry)
 DE Arabidopsis CDPK4 SEQ ID NO 3.
 KW Arabidopsis; CDPK4; calcium dependent protein kinase; oilseed;
 KW disease resistance; agricultural; pathogen; crop yield; ornamental;
 KW fungicide; bactericide; nematocide; insecticide; viroicide; cereal;
 KW transgenic; plant; enzyme.
 OS Arabidopsis thaliana.
 XX WO200184911-A1.
 PN 15-NOV-2001.
 PD 04-MAY-2001; 2001WO-US14368.
 PF 05-MAY-2000; 2000US-201925P.
 PR (GEO) GEN HOSPITAL CORP.
 PA Sheen J;
 PI MPI; 2002-062179/08.
 PS N-PSDB; ABA06022.
 XX Producing plant having increased disease resistance, comprises
 PT regenerating plant from a non-naturally occurring plant cell
 PT over-expressing a polynucleotide encoding a calcium dependent protein
 PT kinase polypeptide -
 XX Disclosure; Fig 2; 44pp; English.

CC The invention relates to producing a plant having increased disease
 CC resistance, comprising providing a non-naturally occurring plant cell
 CC over-expressing a polynucleotide encoding a calcium dependent protein
 CC kinase (CDPK) polypeptide and regenerating a plant from the plant
 CC cell, where the CDPK polypeptide is expressed in the plant, increasing
 CC the resistance of the plant to disease as compared to a naturally-
 CC naturally-occurring plant. The method is useful for a variety of
 CC agricultural and commercial purposes including improving a plant's

CC resistance against plant pathogens, increasing crop yields, improving
 CC crop and ornamental quality and reducing agricultural production costs.
 CC The method facilitates an effective and economical method for in-plant
 CC protection against plant pathogen, reducing or minimising the need for
 CC traditional chemical practices (e.g. application of fungicides,
 CC bactericides, nematocides, insecticides, or viricides) that are typically
 CC used by farmers for controlling the spread of plant pathogens and
 CC providing protection against disease causing pathogens. The method
 CC contributes to the production of high quality and high yield agricultural
 CC products, e.g. fruits, ornamentals, vegetables, cereals and field crops
 CC having reduced spots, blemishes and blotches that are caused by
 CC pathogens, agricultural products with increased shelf-life and reduced
 CC handling costs and high quality and yield crops for agricultural
 CC (e.g. cereal and field crops), industrial (e.g. oilseeds) and commercial
 CC thaliana CDPK4 of the invention.

XX
 QY Sequence 501 AA;
 Query Match 94.8%; Score 2458; DB 23; Length 501;
 Best Local Similarity 94.8%; Pred. No. 2.2e-210;
 Matches 470; Conservative 9; Mismatches 13; Indels 4; Gaps 1;

QY 4 KPNRRPSENTVLPYOTPRLRDHYLLGKLGQGGFGTTYLCTEKSTSANVACKSIPKRLV 63
 DB 3 KPNRRPSENTVLPYOTPRLRDHYLLGKLGQGGFGTTYLCTEKSTSANVACKSIPKRLV 62
 QY 64 CREDYEDVWREIQIMHLSSEHPNVVRIKGTYESVVFHIVMEVCEGELFDRIVSGKFS 123
 DB 63 CREDYEDVWREIQIMHLSSEHPNVVRIKGTYESVVFHIVMEVCEGELFDRIVSGKFS 122
 QY 124 EREAVKLIKTLGVVEACHSIGVMHRLKPENFLFSPKDDAKLKATDFGLSVFYKPGQY 183
 DB 123 EREAVKLIKTLGVVEACHSIGVMHRLKPENFLFSPKDDAKLKATDFGLSVFYKPGQY 182
 QY 184 LYDVVGSPPYVAPVVKCCYCPEDVMSAGVILYLLSGVPEPWAETSGIFRQILQGLK 243
 DB 183 LYDVVGSPPYVAPVVKCCYCPEDVMSAGVILYLLSGVPEPWAETSGIFRQILQGLK 242
 QY 244 DFKSDPWPPTISEAAKDLIYKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAVLSRL 303
 DB 243 DFKSDPWPPTISEGAKDLIYKMLDRSPKKRISAHEALCHPWIVDEHAAPDKPLDPAVLSRL 302
 QY 304 KQFSQMKIKQWALRVIAERLSEEEIGLKLFPKIDTNSGTTITEELKAGLKRYSSEL 363
 DB 303 KQFSQMKIKQWALRVIAERLSEEEIGLKLFPKIDTNSGTTITEELKAGLKRYSSEL 362
 QY 364 MESEIKSLMDAADINSGTIDYGEFLAATLHMKNVREELVAFSDFDKDGSGYITIDE 423
 DB 363 MESEIKSLMDAADINSGTIDYGEFLAATLHMKNVREELVAFSDFDKDGSGYITIDE 422
 QY 424 LOSACTEFGLCDTPLDDMIKEIDLNDGKIDFSEFTAMMKKGDGVGRSRTMRNNLNFNIA 483
 DB 423 LOQACTEFGLCDTPLDDMIKEIDLNDGKIDFSEFTAMMKKGDGVGRSRTMRNNLNFNIA 482
 QY 484 DAFGVDG----EKSD 495
 DB 483 EAFGVEDTSSAKSD 498

RESULT 4
 ID AAG35777 standard; Protein; 425 AA.
 AC AAG35777;
 XX 18-OCT-2000 (first entry)
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 43754.
 KW Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.

XX OS	Arabidopsis thaliana.	PR	29-JUN-1999;	99US-0140991.
XX PN	EPI033405-A2.	PR	30-JUN-1999;	99US-0141287.
XX XX		PR	01-JUL-1999;	99US-0141842.
XX PD	06-SEP-2000.	PR	01-JUL-1999;	99US-0142154.
XX XX		PR	02-JUL-1999;	99US-0142055.
XX PF		PR	06-JUL-1999;	99US-0142390.
XX XX		PR	08-JUL-1999;	99US-0142803.
XX XX		PR	09-JUL-1999;	99US-0142920.
XX XX		PR	12-JUL-1999;	99US-0142977.
XX XX		PR	13-JUL-1999;	99US-0143542.
XX XX		PR	14-JUL-1999;	99US-0143624.
XX XX		PR	15-JUL-1999;	99US-0144085.
XX XX		PR	16-JUL-1999;	99US-0144085.
XX XX		PR	18-JUL-1999;	99US-0144325.
XX XX		PR	19-JUL-1999;	99US-0144331.
XX XX		PR	19-JUL-1999;	99US-0144332.
XX XX		PR	19-JUL-1999;	99US-0144333.
XX XX		PR	19-JUL-1999;	99US-0144334.
XX XX		PR	19-JUL-1999;	99US-0144335.
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XX XX		PR	20-JUL-1999;	99US-0144884.
XX XX		PR	21-JUL-1999;	99US-0144814.
XX XX		PR	21-JUL-1999;	99US-0145086.
XX XX		PR	21-JUL-1999;	99US-0145088.
XX XX		PR	22-JUL-1999;	99US-0145085.
XX XX		PR	22-JUL-1999;	99US-0145087.
XX XX		PR	22-JUL-1999;	99US-0145089.
XX XX		PR	22-JUL-1999;	99US-0145192.
XX XX		PR	23-JUL-1999;	99US-0145145.
XX XX		PR	23-JUL-1999;	99US-0145218.
XX XX		PR	23-JUL-1999;	99US-0145224.
XX XX		PR	25-JUL-1999;	99US-0145276.
XX XX		PR	27-JUL-1999;	99US-0145913.
XX XX		PR	27-JUL-1999;	99US-0145918.
XX XX		PR	27-JUL-1999;	99US-0145918.
XX XX		PR	28-JUL-1999;	99US-0145951.
XX XX		PR	02-AUG-1999;	99US-0146388.
XX XX		PR	02-AUG-1999;	99US-0146389.
XX XX		PR	03-AUG-1999;	99US-0147038.
XX XX		PR	04-AUG-1999;	99US-0147204.
XX XX		PR	04-AUG-1999;	99US-0147302.
XX XX		PR	05-AUG-1999;	99US-0147192.
XX XX		PR	05-AUG-1999;	99US-0147260.
XX XX		PR	06-AUG-1999;	99US-0147303.
XX XX		PR	06-AUG-1999;	99US-0147416.
XX XX		PR	09-AUG-1999;	99US-0147493.
XX XX		PR	09-AUG-1999;	99US-0147935.
XX XX		PR	10-AUG-1999;	99US-0148171.
XX XX		PR	10-AUG-1999;	99US-0148319.
XX XX		PR	12-AUG-1999;	99US-0148341.
XX XX		PR	13-AUG-1999;	99US-0148565.
XX XX		PR	13-AUG-1999;	99US-0148684.
XX XX		PR	16-AUG-1999;	99US-0149368.
XX XX		PR	17-AUG-1999;	99US-0149175.
XX XX		PR	18-AUG-1999;	99US-0149426.
XX XX		PR	20-AUG-1999;	99US-0149723.
XX XX		PR	20-AUG-1999;	99US-0149929.
XX XX		PR	23-AUG-1999;	99US-0149902.
XX XX		PR	23-AUG-1999;	99US-0149930.
XX XX		PR	25-AUG-1999;	99US-0150566.
XX XX		PR	26-AUG-1999;	99US-0150884.
XX XX		PR	27-AUG-1999;	99US-0151065.
XX XX		PR	27-AUG-1999;	99US-0151066.
XX XX		PR	27-AUG-1999;	99US-0151080.
XX XX		PR	30-AUG-1999;	99US-0151303.
XX XX		PR	31-AUG-1999;	99US-0151438.
XX XX		PR	01-SEP-1999;	99US-0151920.
XX XX		PR	07-SEP-1999;	99US-0152363.
XX XX		PR	10-SEP-1999;	99US-0153070.

PR	13-SEP-1999;	99US-0153758.	
PR	15-SEP-1999;	99US-0154018.	
PR	16-SEP-1999;	99US-0154039.	
PR	20-SEP-1999;	99US-0154779.	
PR	22-SEP-1999;	99US-0155139.	
PR	23-SEP-1999;	99US-0155486.	
PR	24-SEP-1999;	99US-0155659.	
PR	28-SEP-1999;	99US-0156458.	
PR	29-SEP-1999;	99US-0156596.	
PR	04-OCT-1999;	99US-0157117.	
PR	05-OCT-1999;	99US-0157753.	
PR	06-OCT-1999;	99US-0157865.	
PR	07-OCT-1999;	99US-0158029.	
PR	08-OCT-1999;	99US-0158232.	
PR	12-OCT-1999;	99US-0158369.	
PR	13-OCT-1999;	99US-0159293.	
PR	13-OCT-1999;	99US-0159294.	
PR	13-OCT-1999;	99US-0159295.	
PR	14-OCT-1999;	99US-0159329.	
PR	14-OCT-1999;	99US-0159330.	
PR	14-OCT-1999;	99US-0159331.	
PR	14-OCT-1999;	99US-0159637.	
PR	14-OCT-1999;	99US-0159638.	
PR	18-OCT-1999;	99US-0159584.	
PR	21-OCT-1999;	99US-0160741.	
PR	21-OCT-1999;	99US-0160767.	
PR	21-OCT-1999;	99US-0160768.	
PR	21-OCT-1999;	99US-0160770.	
PR	21-OCT-1999;	99US-0160814.	
PR	21-OCT-1999;	99US-0160815.	
PR	22-OCT-1999;	99US-0160980.	
PR	22-OCT-1999;	99US-0160981.	
PR	22-OCT-1999;	99US-0160989.	
PR	25-OCT-1999;	99US-0161404.	
PR	25-OCT-1999;	99US-0161405.	
PR	25-OCT-1999;	99US-0161406.	
PR	26-OCT-1999;	99US-0161359.	
PR	26-OCT-1999;	99US-0161360.	
PR	26-OCT-1999;	99US-0161361.	
PR	28-OCT-1999;	99US-0161920.	
PR	28-OCT-1999;	99US-0161992.	
PR	28-OCT-1999;	99US-0161993.	
PR	29-OCT-1999;	99US-0162142.	
Query Match 79.6%; Score 2064; DB 21; Length 425;			
Best Local Similarity 94.5%; Pred. No. 2.4e-175;			
Matches 399; Conservative 6; Mismatches 13; Indels 4; Gaps 1;			
QY	78	MHLSEHPNVRIKGYEDSVFVHIVMEYCEGGELFDRIVSKGHFSEREAYKLKILGV	137
DB	1	MHLSEHPNVRIKGYEDSVFVHIVMEYCEGGELFDRIVSKGHFSEREAYKLKILGV	60
QY	138	VEACHSLGWHRDLKPENFLFDSPKDDAKLKATDGLSVFYKPGQYLDVVGSPYVAPE	197
DB	61	VEACHSLGWHRDLKPENFLFDSPKDDAKLKATDGLSVFYKPGQYLDVVGSPYVAPE	120
QY	198	VLKCKYGPEDVMSAGVILYLLSGVPPWATESGIFRQILQGLDKFSPWPTISEAA	257
DB	121	VLKCKYGPEDVMSAGVILYLLSGVPPWATESGIFRQILQGLDKFSPWPTISEGA	180
QY	258	KDIYKXKLSPKKRISAHEALCHPWIIVDEQAAPDKPLDPAVLSLKQFSQNNKIKQVAL	317
DB	181	KDIYKXKLSPKKRISAHEALCHPWIIVDEQAAPDKPLDPAVLSLKQFSQNNKIKQVAL	240
QY	318	RVTARLSSEIEGLKELFKWIDTNSGTTTPEELKAGLKRVSSELMSEIKSLMDAADI	377
DB	241	RVTARLSSEIEGLKELFKWIDTNSGTTTPEELKAGLKRVSSELMSEIKSLMDAADI	300
QY	378	DNSGTIDYGEFLAATLHMNKNREBEILVAFSPDKDGSYITIDELQACTEFGLCPTP	437
DB	301	DNSGTIDYGEFLAATLHMNKNREBEILVAFSPDKDGSYITIDELQACTEFGLCPTP	360
QY	438	LDDMIKEIDLNDGKIDFSEFTAMMKGGVGRSRTMRNLFNFIABFGVEDTSSTAKS	493

DB	361	LDDMIKEIDLNDGKIDFSEFTAMMKGGVGRSRTMRNLFNFIABFGVEDTSSTAKS	420
QY	494	DD 495	
DB	421	DD 422	
RESULT 5			
ID	AAW93256	standard; Protein; 512 AA.	
XX	AAW93256;		
XX	25-AUG-1999	(first entry)	
XX	Soybean CDPK protein.		
KW	CDPK; calcium dependent protein kinase; tobacco; pathogen; invasion;		
KW	induction; elicitor; plant; disease resistance; parasiticein; soybean;		
KW	elicitin.		
XX	Glycine max.		
PH	Key	Location/Qualifiers	
FT	Region	41..46	
FT	Region	/note= "protein kinase sequence"	
FT	Region	158..163	
FT	Region	/note= "protein kinase sequence"	
FT	Region	198..205	
FT	Region	/note= "protein kinase sequence"	
FT	Binding-site	348..360	
FT	Binding-site	/note= "calcium binding site"	
FT	Binding-site	388..399	
FT	Binding-site	/note= "calcium binding site"	
FT	Binding-site	425..435	
FT	Binding-site	/note= "calcium binding site"	
FT	Binding-site	458..468	
FT	Binding-site	/note= "calcium binding site"	
XX	WO9902655-A1.		
XX	21-JAN-1999.		
XX	07-JUL-1998;	98WO-US14109.	
XX	08-JUL-1997;	97US-0889655.	
XX	(KENT) UNIV KENTUCKY RES FOUND.		
XX	Chappell J, Lusso MFG;		
XX	WPI; 1999-120859/10.		
XX	New polynucleotides based on calcium dependent protein kinase genes		
XX	- useful to induce disease resistance in plants		
XX	Example 4; Fig 4; Sipp; English.		
XX	This invention describes a novel nucleic acid molecule and its encoded		
XX	protein that are induced upon pathogen invasion or elicitor treatment.		
XX	The products of the invention are functional in plants, plant tissue and		
XX	in plant cells for inducible gene expression and altering the disease		
XX	resistance phenotype of plants. The products of the invention are		
XX	related to calcium dependent protein kinase (CDPK) genes. The invention		
XX	describes the isolation of a novel tobacco CDPK protein fragment and its		
XX	encoding nucleic acid, isolated from a cell suspension culture derived		
XX	from a tobacco cultivar K14 explant, after growth in the presence of		
XX	the elicitor parasiticein. This sequence represents the soybean CDPK		
XX	protein which is used in the description of the method.		
XX	Sequence	512 AA;	

Query Match		74.5%	Score 1932	DB 20	Length 512	
Best Local Similarity		77.1%	Pred. No. 1.9e-163			
Matches 370		Conservative 51	Mismatches 51	Indels 8	Gaps 4	
OY	14	VLPQTPRDRDHYLLKGLQGQFGTTLCTEKTSTSANVACKSIIPKRLVKREDYEDVWR	73			
DB	22	VLPQTNIREVVEGRKLQGQFGTTFCTRASGGKFAKSIIPKRLKCKEDYEDVWR	81			
OY	74	EIOIMHLSHPNVVRIKITYEDSVFVHIVMEVCEGGLFDRIVSKGHFSREAVKLIKT	133			
DB	82	EIOIMHLSHANVRIEGTYEDSTAVHIVMLCEGGLFDRIVQKHYSERQARLIKT	141			
OY	134	ILGVWACHSLGVMHRLKPNFLDSPDKAKLATDGLSVFYKPGGYLYDVVVGSPYY	193			
DB	142	IVFVWACHSLGVMHRLKPNFLFTIDEDAKLATDGLSVFYKPGESFCDVVGSPYY	201			
OY	194	VAPEVLKCCVGPIDVMSAGVILYILSGVPPFWAFTESGIFRQILQKGLDPKSDPWTI	253			
DB	202	VAPEVLKLYGPESDVMSAGVILYILSGVPPFWAFTESGIFRQILGLKDFHSEFPESI	261			
OY	254	SEAKDILYKWLSPKRTISAHEALCHPWIVDEQAAPKPLDPAVLRLKQFOSOMNIK	313			
DB	262	SDSAKDILRKWLQONPKRTUTAEVLRHFWIVDDNIAPKPLDSAVLSLKQFSAMNKLK	321			
OY	314	KMALRVIAERLSEEEIGGLKELFKMIDTNSGTTITPEE---LKAGLKVGSSELMSEIK	369			
DB	322	KMALRVIAERLSEEEIGGLKELFKMIDTNSGTTITPELKDGLKDKLKVGSSELMSEIK	381			
OY	370	SLMDAADINSGTIDYGEFLAATLHMKNWEREILVAEFDKDGSGVITIDELOSACT	429			
DB	382	DLMDAADINSGTIDYGEFLAATVHLNKREENLVSAFSYFDKDGSGVITIDEQQACK	441			
OY	430	EFGLCDTPELDMIKEIDLDNDGKIDFSEFTAMVRKGD-GVGRSRTMMKNLNFNIADFGV	488			
DB	442	DFGLDDDIHIDDMIKEIDQDNDGQIDYGEFAAMVRKNGGIGR-RTWRKTL--NLRDALGL	498			
RESULT 6						
AAG35778						
ID	AAG35778 standard; Protein; 399 AA.					
XX	AAG35778;					
AC	AAG35778;					
XX	18-OCT-2000 (first entry)					
DT	Arabidopsis thaliana protein fragment SEQ ID NO: 43755.					
DE	Arabidopsis thaliana					
XX	Protein identification; signal transduction pathway; metabolic pathway;					
KW	hybridisation assay; genetic mapping; gene expression control; promoter;					
KW	termination sequence.					
XX	Arabidopsis thaliana.					
OS	Arabidopsis thaliana.					
PN	EP1033405-A2.					
XX	06-SEP-2000.					
PD	25-FEB-2000; 2000EP-0301439.					
XX	25-FEB-1999; 99US-0121825.					
PR	05-MAR-1999; 99US-0123180.					
PR	09-MAR-1999; 99US-0123548.					
PR	23-MAR-1999; 99US-0125788.					
PR	25-MAR-1999; 99US-0126264.					
PR	29-MAR-1999; 99US-0126785.					
PR	01-APR-1999; 99US-0127462.					
PR	06-APR-1999; 99US-0128234.					
PR	08-APR-1999; 99US-0128714.					
PR	16-APR-1999; 99US-0129845.					
PR	19-APR-1999; 99US-0130077.					
PR	21-APR-1999; 99US-0130449.					
PR	23-APR-1999; 99US-0130510.					
PR	23-APR-1999; 99US-0130891.					
PR	28-APR-1999; 99US-0131449.					
PR	30-APR-1999; 99US-0132048.					
PR	30-APR-1999; 99US-0132407.					
PR	04-MAY-1999; 99US-0132484.					
PR	05-MAY-1999; 99US-0132485.					
PR	06-MAY-1999; 99US-0132486.					
PR	06-MAY-1999; 99US-0132487.					
PR	07-MAY-1999; 99US-0132863.					
PR	11-MAY-1999; 99US-0134256.					
PR	14-MAY-1999; 99US-0134218.					
PR	14-MAY-1999; 99US-0134219.					
PR	14-MAY-1999; 99US-0134221.					
PR	14-MAY-1999; 99US-0134370.					
PR	18-MAY-1999; 99US-0134768.					
PR	19-MAY-1999; 99US-0134941.					
PR	20-MAY-1999; 99US-0135124.					
PR	21-MAY-1999; 99US-0135353.					
PR	24-MAY-1999; 99US-0135629.					
PR	25-MAY-1999; 99US-0136021.					
PR	27-MAY-1999; 99US-0136392.					
PR	28-MAY-1999; 99US-0136782.					
PR	01-JUN-1999; 99US-0137222.					
PR	03-JUN-1999; 99US-0137528.					
PR	04-JUN-1999; 99US-0137502.					
PR	07-JUN-1999; 99US-0137724.					
PR	08-JUN-1999; 99US-0138094.					
PR	10-JUN-1999; 99US-0138540.					
PR	10-JUN-1999; 99US-0138847.					
PR	14-JUN-1999; 99US-0139119.					
PR	16-JUN-1999; 99US-0139452.					
PR	16-JUN-1999; 99US-0139453.					
PR	17-JUN-1999; 99US-0139492.					
PR	18-JUN-1999; 99US-0139454.					
PR	18-JUN-1999; 99US-0139455.					
PR	18-JUN-1999; 99US-0139456.					
PR	18-JUN-1999; 99US-0139457.					
PR	18-JUN-1999; 99US-0139458.					
PR	18-JUN-1999; 99US-0139459.					
PR	18-JUN-1999; 99US-0139460.					
PR	18-JUN-1999; 99US-0139461.					
PR	18-JUN-1999; 99US-0139462.					
PR	18-JUN-1999; 99US-0139463.					
PR	18-JUN-1999; 99US-0139750.					
PR	18-JUN-1999; 99US-0139763.					
PR	21-JUN-1999; 99US-0139817.					
PR	22-JUN-1999; 99US-0139899.					
PR	23-JUN-1999; 99US-0140353.					
PR	23-JUN-1999; 99US-0140354.					
PR	24-JUN-1999; 99US-0140695.					
PR	28-JUN-1999; 99US-0140823.					
PR	29-JUN-1999; 99US-0140991.					
PR	30-JUN-1999; 99US-0141287.					
PR	01-JUL-1999; 99US-0141842.					
PR	01-JUL-1999; 99US-0142154.					
PR	02-JUL-1999; 99US-0142055.					
PR	06-JUL-1999; 99US-0142390.					
PR	08-JUL-1999; 99US-0142803.					
PR	09-JUL-1999; 99US-0142920.					
PR	12-JUL-1999; 99US-0142977.					
PR	13-JUL-1999; 99US-0143542.					
PR	14-JUL-1999; 99US-0143624.					
PR	15-JUL-1999; 99US-0144005.					
PR	16-JUL-1999; 99US-0144085.					
PR	16-JUL-1999; 99US-0144086.					
PR	19-JUL-1999; 99US-0144325.					
PR	19-JUL-1999; 99US-0144331.					
PR	19-JUL-1999; 99US-0144332.					
PR	19-JUL-1999; 99US-0144333.					
PR	19-JUL-1999; 99US-0144334.					
PR	19-JUL-1999; 99US-0144335.					
PR	20-JUL-1999; 99US-0144352.					
PR	20-JUL-1999; 99US-0144632.					
PR	20-JUL-1999; 99US-0144884.					

XX	PR	25-FEB-2000; 2000EP-0301439.	PR	08-JUL-1999;	99US-0142803.
XX	PR		PR	09-JUL-1999;	99US-0142920.
XX	PR		PR	12-JUL-1999;	99US-0142977.
PR	PR	25-FEB-1999;	PR	13-JUL-1999;	99US-0143542.
PR	PR	99US-0121825.	PR	14-JUL-1999;	99US-0143624.
PR	PR	99US-0123180.	PR	15-JUL-1999;	99US-0144005.
PR	PR	99US-0123548.	PR	16-JUL-1999;	99US-0144085.
PR	PR	99US-0125788.	PR	16-JUL-1999;	99US-0144086.
PR	PR	99US-0126264.	PR	19-JUL-1999;	99US-0144325.
PR	PR	99US-0126785.	PR	19-JUL-1999;	99US-0144331.
PR	PR	99US-0127462.	PR	19-JUL-1999;	99US-0144332.
PR	PR	99US-0128234.	PR	19-JUL-1999;	99US-0144333.
PR	PR	99US-0128714.	PR	19-JUL-1999;	99US-0144334.
PR	PR	99US-0129845.	PR	19-JUL-1999;	99US-0144335.
PR	PR	99US-0130077.	PR	20-JUL-1999;	99US-0144352.
PR	PR	99US-0130449.	PR	20-JUL-1999;	99US-0144632.
PR	PR	99US-0130510.	PR	20-JUL-1999;	99US-0144884.
PR	PR	99US-0130891.	PR	21-JUL-1999;	99US-0144814.
PR	PR	99US-0131449.	PR	21-JUL-1999;	99US-0145086.
PR	PR	99US-0132048.	PR	21-JUL-1999;	99US-0145088.
PR	PR	99US-0132407.	PR	21-JUL-1999;	99US-0145088.
PR	PR	99US-0132484.	PR	22-JUL-1999;	99US-0145088.
PR	PR	99US-0132485.	PR	22-JUL-1999;	99US-0145087.
PR	PR	99US-0132486.	PR	22-JUL-1999;	99US-0145089.
PR	PR	99US-0132487.	PR	22-JUL-1999;	99US-0145192.
PR	PR	99US-0132863.	PR	23-JUL-1999;	99US-0145145.
PR	PR	99US-0132863.	PR	23-JUL-1999;	99US-0145218.
PR	PR	99US-0134256.	PR	23-JUL-1999;	99US-0145224.
PR	PR	99US-0134218.	PR	26-JUL-1999;	99US-0145276.
PR	PR	99US-0134219.	PR	27-JUL-1999;	99US-0145913.
PR	PR	99US-0134221.	PR	27-JUL-1999;	99US-0145918.
PR	PR	99US-0134370.	PR	27-JUL-1999;	99US-0145919.
PR	PR	99US-0134370.	PR	27-JUL-1999;	99US-0145951.
PR	PR	99US-0134768.	PR	28-JUL-1999;	99US-0145951.
PR	PR	99US-0134941.	PR	02-AUG-1999;	99US-0146386.
PR	PR	99US-0135124.	PR	02-AUG-1999;	99US-0146388.
PR	PR	99US-0135353.	PR	02-AUG-1999;	99US-0146389.
PR	PR	99US-0135629.	PR	02-AUG-1999;	99US-0146389.
PR	PR	99US-0136021.	PR	03-AUG-1999;	99US-0147038.
PR	PR	99US-0136392.	PR	04-AUG-1999;	99US-0147204.
PR	PR	99US-0136782.	PR	04-AUG-1999;	99US-0147302.
PR	PR	99US-0137222.	PR	05-AUG-1999;	99US-0147192.
PR	PR	99US-0137528.	PR	05-AUG-1999;	99US-0147260.
PR	PR	99US-0137502.	PR	06-AUG-1999;	99US-0147303.
PR	PR	99US-0137724.	PR	06-AUG-1999;	99US-0147416.
PR	PR	99US-0138094.	PR	09-AUG-1999;	99US-0147493.
PR	PR	99US-0138540.	PR	09-AUG-1999;	99US-0147935.
PR	PR	99US-0138847.	PR	10-AUG-1999;	99US-0148171.
PR	PR	99US-0139119.	PR	11-AUG-1999;	99US-0148319.
PR	PR	99US-0139452.	PR	12-AUG-1999;	99US-0148341.
PR	PR	99US-0139453.	PR	13-AUG-1999;	99US-0148565.
PR	PR	99US-0139492.	PR	13-AUG-1999;	99US-0148684.
PR	PR	99US-0139492.	PR	16-AUG-1999;	99US-0149368.
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PR	PR	99US-0139457.	PR	20-AUG-1999;	99US-0149723.
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PR	PR	99US-0139460.	PR	23-AUG-1999;	99US-0149930.
PR	PR	99US-0139461.	PR	25-AUG-1999;	99US-0150566.
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PR	PR	99US-0139720.	PR	27-AUG-1999;	99US-0151066.
PR	PR	99US-0139763.	PR	27-AUG-1999;	99US-0151080.
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PR	PR	99US-0140334.	PR	07-SEP-1999;	99US-0152363.
PR	PR	99US-0140695.	PR	10-SEP-1999;	99US-0153070.
PR	PR	99US-0140823.	PR	13-SEP-1999;	99US-0153758.
PR	PR	99US-0140951.	PR	15-SEP-1999;	99US-0154018.
PR	PR	99US-0141287.	PR	16-SEP-1999;	99US-0154039.
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PR	PR	99US-0142154.	PR	22-SEP-1999;	99US-0155139.
PR	PR	99US-0142055.	PR	23-SEP-1999;	99US-0155486.
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PR	21-OCT-1999;	99US-0160741.
PR	21-OCT-1999;	99US-0160767.
PR	21-OCT-1999;	99US-0160768.
PR	21-OCT-1999;	99US-0160770.
PR	21-OCT-1999;	99US-0160814.
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PR	22-OCT-1999;	99US-0160981.
PR	22-OCT-1999;	99US-0160989.
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PR	25-OCT-1999;	99US-0161406.
PR	26-OCT-1999;	99US-0161359.
PR	26-OCT-1999;	99US-0161360.
PR	26-OCT-1999;	99US-0161361.
PR	28-OCT-1999;	99US-0161920.
PR	28-OCT-1999;	99US-0161922.
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PR	29-OCT-1999;	99US-0162142.
PR	29-OCT-1999;	99US-0162142.
Query Match 67.2%; Score 1742; DB 21; Length 483;		
Best Local Similarity 68.4%; Pred. No. 1.5e-146;		
Matches 329; Conservative 66; Mismatches 84; Indels 2; Gaps 2;		
QY	6	NPRRSNTVLPVQTPRLRDHYLLGKLGQGGFTTYLCTEKSTANTYACKSIPKRLVCR 65
DB	4	NPDNQAYVVLGHKTNIRDIYTLRSKLGQGGFTTYLCTEIASGVYACKSISKRKLISK 63
QY	66	EYEDVWRRIQIMHLSHPNNVRIKGYEDSVFVHVEYCEGGEFLDRIYVSKGHFSE 125
DB	64	EVEDVRRRIQIMHLAGHSIVTIKGYEDSLYVHVEYCEGGEFLDRIYVSKGHFSE 123
QY	126	EAVKLITLGVVEACHSLGVNMRDLKPNFLFDSKDDAKLKTDFGLSVFYKPGQYLY 185
DB	124	KAELTKIIVGVVEACHSLGVNMRDLKPNFLFVNKDDDFSLKAIDFGLSVFYKPGQY 183
QY	186	DVVGSPYVAPVPELKKVCGPETDVMSAGVILYLLSGVPPWAETESGIPQILQGLDF 245
DB	184	DVVGSPYVAPVPELKKVCGPETDVMSAGVILYLLSGVPPWAETESGIPQILQGLDF 243
QY	246	KSDPWPTEISAAKDLIYKMLERSPKKRISAHEALCHPNIVDEQAAPKPLPAVLSLKQ 305
DB	244	ESDPWPTEISAAKDLIYKMLERSPKKRISAHEALCHPNIVDEQAAPKPLPAVLSLKQ 303
QY	306	FSQWNIKKWALVIAERLSEIEIGLKFEMIDTNSGTTTPEELKAGLKRYGSELME 365
DB	304	FSQWNIKKWALVIAERLSEIEIGLKFEMIDTNSGTTTPEELKAGLKRYGSELME 363
QY	366	SEIKSLMDADIINSGTIDYGEFLAATLHMNKREREELIVAAFSDFDKGSGYITIDELQ 425
DB	364	TEIHLMDAADVNSGTIDYSEFIATIHNLKEREHLVAAQVFDKDGSGYITIDELQ 423
QY	426	SACTEFLGCTPLDNNKIDLDNDKIDFSEFTAMRKGCD-GVGRSRMTMKQNFNFIAD: 484
DB	424	QACVEHGMADVFLIEDIKYQDNDKIDYGEFVEMVQKGNAGVGR-RTMNRSLNISMRD 482

QY	485 A 485
DB	483 A 483
RESULT 8	
AAG31157	
ID	AAG31157 standard; Protein; 556 AA.
XX	AC
XX	AAG31157;
DT	17-OCT-2000 (first entry)
DE	Arabidopsis thaliana protein fragment SEQ ID NO: 37371.
KW	Protein identification; signal transduction pathway; metabolic pathway;
KW	hybridisation assay; genetic mapping; gene expression control; promoter;
KW	termination sequence.
OS	Arabidopsis thaliana.
XX	EP1033405-A2.
XX	06-SEP-2000.
XX	25-FEB-2000; 2000EP-0301439.
XX	25-FEB-1999; 99US-0121825.
XX	03-MAR-1999; 99US-012180.
XX	23-MAR-1999; 99US-0123548.
XX	23-MAR-1999; 99US-0125788.
XX	23-MAR-1999; 99US-0126264.
XX	29-MAR-1999; 99US-0126785.
XX	01-APR-1999; 99US-0127462.
XX	06-APR-1999; 99US-0128234.
XX	08-APR-1999; 99US-0128714.
XX	16-APR-1999; 99US-0129845.
XX	19-APR-1999; 99US-0130077.
XX	21-APR-1999; 99US-0130449.
XX	23-APR-1999; 99US-0130510.
XX	23-APR-1999; 99US-0130891.
XX	28-APR-1999; 99US-0131449.
XX	30-APR-1999; 99US-0132048.
XX	30-APR-1999; 99US-0132407.
XX	04-MAY-1999; 99US-0132484.
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XX	11-MAY-1999; 99US-0134256.
XX	14-MAY-1999; 99US-0134318.
XX	14-MAY-1999; 99US-0134319.
XX	14-MAY-1999; 99US-0134321.
XX	14-MAY-1999; 99US-0134370.
XX	18-MAY-1999; 99US-0134768.
XX	19-MAY-1999; 99US-0134941.
XX	20-MAY-1999; 99US-0135124.
XX	21-MAY-1999; 99US-0135353.
XX	24-MAY-1999; 99US-0135623.
XX	25-MAY-1999; 99US-0136021.
XX	27-MAY-1999; 99US-0136392.
XX	28-MAY-1999; 99US-0136782.
XX	01-JUN-1999; 99US-0137222.
XX	03-JUN-1999; 99US-0137528.
XX	04-JUN-1999; 99US-0137502.
XX	07-JUN-1999; 99US-0137724.
XX	08-JUN-1999; 99US-0138094.
XX	10-JUN-1999; 99US-0138540.
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XX	16-JUN-1999; 99US-0139452.
XX	16-JUN-1999; 99US-0139453.

PR 17-JUN-1999; 99US-0139492.
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 PR 01-JUL-1999; 99US-0142154.
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 PR 08-JUL-1999; 99US-0142803.
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 PR 12-JUL-1999; 99US-0142977.
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 PR 27-JUL-1999; 99US-0145919.
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 PR 02-AUG-1999; 99US-0146389.
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 PR 04-AUG-1999; 99US-0147204.
 PR 04-AUG-1999; 99US-0147302.
 PR 05-AUG-1999; 99US-0147192.
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 PR 06-AUG-1999; 99US-0147416.
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 PR 10-AUG-1999; 99US-0148171.
 PR 11-AUG-1999; 99US-0148319.
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 PR 13-AUG-1999; 99US-0148565.

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 PR 17-AUG-1999; 99US-0149359.
 PR 18-AUG-1999; 99US-0149446.
 PR 20-AUG-1999; 99US-0149722.
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 PR 23-AUG-1999; 99US-0149902.
 PR 23-AUG-1999; 99US-0149930.
 PR 25-AUG-1999; 99US-0150566.
 PR 26-AUG-1999; 99US-0150884.
 PR 27-AUG-1999; 99US-0151065.
 PR 27-AUG-1999; 99US-0151066.
 PR 27-AUG-1999; 99US-0151080.
 PR 30-AUG-1999; 99US-0151303.
 PR 31-AUG-1999; 99US-0151438.
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 PR 07-SEP-1999; 99US-0152363.
 PR 10-SEP-1999; 99US-0153070.
 PR 13-SEP-1999; 99US-0153758.
 PR 16-SEP-1999; 99US-0154018.
 PR 20-SEP-1999; 99US-0154779.
 PR 22-SEP-1999; 99US-0155139.
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 PR 24-SEP-1999; 99US-0155559.
 PR 28-SEP-1999; 99US-0156458.
 PR 29-SEP-1999; 99US-0156596.
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 PR 05-OCT-1999; 99US-0157753.
 PR 06-OCT-1999; 99US-0157865.
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 PR 26-OCT-1999; 99US-0161361.
 PR 28-OCT-1999; 99US-0161920.
 PR 28-OCT-1999; 99US-0161922.
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 PR 29-OCT-1999; 99US-0162142.

Query Match 67.2%; Score 1742; DB 21; Length 556;
 Best Local Similarity 68.4%; Pred. No. 1.9e-146;
 Matches 329; Conservative 66; Mismatches 84; Indels 2; Gaps 2;
 QY 6 NRRPSTVLPYOTPLRDRHYLLGKLGQGGTTLCTEKTSTANYACKSIPKRLVCR 65
 DB 77 NPDNQAYVVLGHKTPNIRDIYTLRSKLGQGGTTLCTETIASGVYACKSISKRLISK 136
 QY 66 EDYEDYWRREIQIWHLSEHPNVRIKGTYESVVFHVIVMEVCEGGEFDRIVSKGHFSER 125

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PR	23-JUL-1999;	99US-0145218.
PR	23-JUL-1999;	99US-0145224.
PR	26-JUL-1999;	99US-0145276.
PR	27-JUL-1999;	99US-0145913.
PR	27-JUL-1999;	99US-0145918.
PR	27-JUL-1999;	99US-0145919.
PR	28-JUL-1999;	99US-0145951.
PR	02-AUG-1999;	99US-0145386.
PR	02-AUG-1999;	99US-0145388.
PR	02-AUG-1999;	99US-0145389.
PR	03-AUG-1999;	99US-0147038.
PR	04-AUG-1999;	99US-0147204.
PR	05-AUG-1999;	99US-0147302.
PR	05-AUG-1999;	99US-0147192.
PR	05-AUG-1999;	99US-0147260.
PR	06-AUG-1999;	99US-0147303.
PR	06-AUG-1999;	99US-0147416.
PR	09-AUG-1999;	99US-0147493.
PR	09-AUG-1999;	99US-0147935.
PR	10-AUG-1999;	99US-0148171.
PR	11-AUG-1999;	99US-0148319.
PR	12-AUG-1999;	99US-0148341.
PR	13-AUG-1999;	99US-0148565.
PR	13-AUG-1999;	99US-0148684.
PR	16-AUG-1999;	99US-0149368.
PR	17-AUG-1999;	99US-0149175.
PR	18-AUG-1999;	99US-0149426.
PR	20-AUG-1999;	99US-0149722.
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PR	20-AUG-1999;	99US-0149829.
PR	23-AUG-1999;	99US-0149902.
PR	23-AUG-1999;	99US-0149930.
PR	25-AUG-1999;	99US-0150566.
PR	26-AUG-1999;	99US-0150884.
PR	27-AUG-1999;	99US-0151065.
PR	27-AUG-1999;	99US-0151066.
PR	27-AUG-1999;	99US-0151080.
PR	30-AUG-1999;	99US-0151303.
PR	31-AUG-1999;	99US-0151438.
PR	01-SEP-1999;	99US-0151930.
PR	10-SEP-1999;	99US-0152363.
PR	10-SEP-1999;	99US-0153070.
PR	13-SEP-1999;	99US-0153758.
PR	15-SEP-1999;	99US-0154018.
PR	16-SEP-1999;	99US-0154039.
PR	20-SEP-1999;	99US-0154779.
PR	22-SEP-1999;	99US-0155139.
PR	23-SEP-1999;	99US-0155486.
PR	24-SEP-1999;	99US-0155659.
PR	28-SEP-1999;	99US-0156458.
PR	29-SEP-1999;	99US-0156596.
PR	04-OCT-1999;	99US-0157117.
PR	06-OCT-1999;	99US-0157753.
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PR	08-OCT-1999;	99US-0158232.
PR	12-OCT-1999;	99US-0158369.
PR	13-OCT-1999;	99US-0159293.
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PR	26-OCT-1999;	99US-0161360.
PR	26-OCT-1999;	99US-0161361.
PR	28-OCT-1999;	99US-0161920.
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PR	29-OCT-1999;	99US-0162142.
Query Match 65.7%; Score 1703; DB 21; Length 856;		
Best Local Similarity 65.7%; Pred. No. 1e-142;		
Matches 323; Conservative 64; Mismatches 81; Indels 24; Gaps 2;		
QY	2	ETKPNRRP-----SNTVLPYQTPRLADHYLLGKLGQGGQFGTTLCTEKSTS 49
DB	348	ETKAEFPQPKPMRRVSSAGLRTESVLQRKTENKFYSLGRKLGQGGQFGTTLCTEKSTS 407
QY	50	ANYACKSIPKRLVCREDYEDVWREIQIMHLSHPNVVRIKGYEDSVFVHIVNEVCEG 109
DB	408	NEYACKSISKRKLLTDEDVEDVRREIQIMHLAGHPNVISIKGAYEDVVAHLYNELCSG 467
QY	110	GELFDRIVSKGHFSEREAVKLKTLGVVEACHSILGVWHRDLKPNFLFDSFKDADAKA 169
DB	468	GELFDRIIQORHYTERKAELARTIVGLEACHSLGVWHRDLKPNFLFVSREDSLLKT 527
QY	170	TDGLSVFYKPGQYLYDVVGSPPYVAPEVLKCKYGEIDVMSAGVILYLLSGVPPFWA- 228
DB	528	IDFGLSNFFKPDVEFTDVVGSPPYVAPEVLKRYGPESDVMSAGVIVVILLSGVPPFWAG 587
QY	229	-----ETESGIFRQILOGKLDKSDPWPITISAAKDLIKMLERSPKKEISAHE 277
DB	588	SEYNLFMSKYTEQGIPEQVLUHGLDFSSDPWPSISAKDLVKRMLVRDPKRLTDAHQ 647
QY	278	ALCHPMIVDEQAAPDKPLDPAVLSRLKQFSQMNKTKQALRVIAERLSEEEIGGKELFK 337
DB	648	VLCHPNVQIDGVAPDKPLDSAVLSRMKQFSANMKFKKVALAVIAESLSEEEIAGLKQMFK 707
QY	338	MIDTNSGTTTFEELKAGLKRVGSELMSEIKSLMDAADIDNSGTIDYGEFLAATLHVK 397
DB	708	MIDADNSGQITFEELKAGLKRVGANLKESEILDLMQAADVDNSGTIDYKEFTAAATLHVK 767
QY	398	MESEELVAAFSDFDXDGSYITIDELQACTEFGLCDTPLDDMIKEIDLNDGKIDFSE 457
DB	768	IEREDHLFAAFSYFDKDESGFITPDELQACCEFGVEDARIEEMRDVDQDKGRIDYNE 827
QY	458	FTAMMRKGDGVG 469
DB	828	FVAMMQKGSIMG 839
RESULT 10		
AAG38598		
ID AAG38598 standard; Protein; 893 AA.		
XX	AC	AAG38598;
XX	AC	AAG38598;
DT	18-OCT-2000	(first entry)
XX	Arabidopsis thaliana	protein fragment SEQ ID NO: 47641.
XX	Arabidopsis thaliana	protein identification; signal transduction pathway; metabolic pathway;
KW	hybridisation assay;	genetic mapping; gene expression control; promoter;
KW	termination sequence.	
XX	Arabidopsis thaliana.	
OS	Arabidopsis thaliana.	
XX	EP1033405-A2.	

QY 50 ANYACKSIPEKLVCREDEYVMEKREIQIMHLSHPNVVRIKGTVEDGVFVHVMVECEG 109
DB 569 NEVACKSISKKLLTDEVEDVREIQIMHLAGPNVISIKGAYEDVVAHLVVELCSG 628
QY 110 GELFDRIYKGFSESEAVKILKILGVVEACHSLGWHRDLKPNFLDFSPKDDAKKA 169
DB 629 GELFDRIYKGFSESEAVKILKILGVVEACHSLGWHRDLKPNFLDFVSEEDSLKT 688
QY 170 TDGLSVFYKPGGVYDVVGVSPYVVAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWA- 228
DB 689 IDGLSWFFKPDVDFDVGVSPYVVAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAG 748
QY 229 -----ETESGIFRQILQGLKDFKSDPWTISEAAKOLIYKMLERSPKRISAE 277
DB 749 SEVNLFSMKYTETEQIGFQVLHGLDLDGSSDWPSSSESAXDLVRKMLVROPKRLTAHQ 808
QY 278 ALCHPWIVDEQAPDPLPAVLSRLKQSQVNIKKMRLVIAERLSEEBTGGIKLFFK 337
DB 809 VLCHPWVQIDGVAPDPLPAVLSRLKQSQVNIKKMRLVIAERLSEEBTGGIKLFFK 368
QY 338 MIDTNSGTTTFEELKAGLRKVGSELMSESEIKSLMDAADINDSGTIDYGEFLAATLHMK 397
DB 869 MIDADNSGTTTFEELKAGLRKVGSELMSESEIKSLMDAADINDSGTIDYGEFLAATLHMK 928
QY 398 MERBEILVAAPDFDKDGSYITIDELQACTEFGCLDPLDDMIKEIDLNDGKIDFSE 457
DB 929 IEREDHLFAAFSYFDKDSGFIPTDELQACEFGEVDARIBEMMRDQVDDQKGRIDINE 988
QY 458 FTAMWRKGDGVG 469
DB 989 FVAMWQKGSIMG 1000
RESULT 12
AAW52842
ID AAW52842 standard; Protein; 549 AA.
XX
AC AAW52842;
XX
DT 22-FEB-2002 (first entry)
XX
DE Physcomitrella patens CPK-2 protein, SEQ ID NO:39.
XX
KW Protein kinase stress-related protein; PKSRP; moss; protein kinase-6;
KW PK-6; protein kinase-7; PK-7; protein kinase-8; PK-8; protein kinase-9;
KW PK-9; casein kinase homologue-1; CK-1; casein kinase homologue-2; CK-2;
KW casein kinase homologue-3; CK-3; mitogen-activated protein kinase;
KW MAP kinase-2; MPK-2; MAP kinase-3; MPK-3; MAP kinase-4; MPK-4;
KW MAP kinase-5; MPK-5; calcium-dependent protein kinase-1; CPK-1;
KW calcium-dependent protein kinase-2; CPK-2; overexpression;
KW environmental stress; salinity; drought; temperature; tolerance;
KW transgenic plant; EST; expressed sequence tag.
XX
OS Physcomitrella patens.
XX
FN WO200177356-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-US11435.
XX
PR 07-APR-2000; 2000US-196001P.
XX
PA (BADI) BASF PLANT SCI GMBH.
XX
PI Da Costa Silva EO, Bohnert HJ, Van Thielens N, Chen R;
PI Sarria-Millan R;
XX
DR WPI; 2002-049153/06.
XX
PT N-PSDB; ABA91081.
XX
PT New protein, useful for increasing tolerance to environmental stress,
PT comprises a Protein Kinase Stress-Related Protein selected from

PT Protein kinases, Casein kinase homologs, MAP kinases or Calcium
PT dependent protein kinases
XX
PS Claim 13; Fig 3M; 154pp; English.
XX
CC Sequences AAW52830-AAW52842 represent novel protein kinase stress-related
CC proteins (PKSRPs) from the moss Physcomitrella patens, and sequences
CC ABA91069-ABA91081 represent full-length cDNAs encoding them. The cDNA
CC sequences were obtained from expressed sequence tags (ESTs; ABA91056-
CC ABA91068) derived from Physcomitrella patens cDNA libraries. The PKSRPs
CC of the invention comprise protein kinase-6 (PK-6), protein kinase-7
CC (PK-7), protein kinase-8 (PK-8), protein kinase-9 (PK-9), casein kinase
CC homologue-1 (CK-1), casein kinase homologue-2 (CK-2), casein kinase
CC homologue-3 (CK-3), mitogen-activated protein (MAP) kinase-2 (MPK-2),
CC MAP kinase-3 (MPK-3), MAP kinase-4 (MPK-4), MAP kinase-5 (MPK-5),
CC calcium-dependent protein kinase-1 (CPK-1), and calcium-dependent protein
CC kinase-2 (CPK-2). When overexpressed, the PKSRPs are able to confer
CC tolerance to environmental stresses such as salinity, drought,
CC temperature, metal, chemical, pathogenic and oxidative stress.
CC Physcomitrella patens PKSRP nucleic acids may be used to generate
CC transgenic plants and seeds with increased tolerance to salinity, drought
CC and temperature. The transgenic plants generated can be monocots or
CC dicots and are especially maize, wheat, rice, oat, triticale, rice,
CC barley, cotton, rapeseed, cassava, sunflower, tagetes, leguminous plants
CC (e.g., soybean, peanut, Vicia species, alfalfa), solanaceous plants
CC (e.g., potato, tobacco, aubergine, pepper, tomato), coffee, cacao, tea,
CC Salix species, oil palm, coconut, perennial grasses and forage crops. The
CC PKSRP nucleotide and proteins may also be used in evolutionary and
CC protein structural studies and as markers for specific regions of
CC the genome.
XX
SQ Sequence 549 AA;
Query Match 58.2%; Score 1509.5; DB 23; Length 549;
Best Local Similarity 60.8%; Pred. No. 9.9e-126;
Matches 290; Conservative 70; Mismatches 112; Indels 5; Gaps 3;
QY 5 PNPRLPSNT---VLPYQTPRLDRHYLLKGLKGGQFGTTLCTEKTSTANTYACKSIKRRK 61
DB 69 PRPKPASRSVSGVLGKPLSDIRQSYILGRELGGQFGVTYLTCDQMTNEAYACKSIKRRK 128
QY 62 LVCREDEYVMEKREIQIMHLSHPNVVRIKGTVEDGVFVHVMVECEGELFDRIYVSKGH 121
DB 129 LTSKEIDYKREYQIMHLSHPNVVRIKGTVEDGVFVHVMVECEGELFDRIYVSKGH 189
QY 122 FSRREAVKILKILGVVEACHSLGWHRDLKPNFLDFSPKDDAKKATDFGLSVFYKPG 181
DB 189 YSERRAADMCRLVNVVHCHSLGVPHRDLKPNFLDLKAEADAPLKATDFGLSTFFKPG 248
QY 182 QYLYDVVGVSPYVVAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFRQILQ 241
DB 249 DVFDIVGSAYVVAPEVLKCYGPEADVWSAGVIVVILLCGVPPFWAETEOGIFDAVLKG 308
QY 242 KLDPKSDPWTISEAAKOLIYKMLERSPKRISAEALCHPWIVDEQAPDPLPAVLS 301
DB 309 HIDPENDPWPKISNGAKDLVRKMLNPNVKIRLTAQVNLNHPMKEDGADPVDLNAVLT 368
QY 302 RLKQFSQMNKIKVMAERLSEEBTGGIKLFFKIDTNSGTITFEELKAGLRKVGVS 361
DB 369 RLKNFSAANKMKXALKVIAESLSEEBTGGIKLFFKIDTNSGTITFEELKAGLRKVGVS 428
QY 362 ELMESEIKSLMDAADINDSGTIDYGEFLAATLHMKWREBEILVAAPDFDKDGSYITI 421
DB 429 KLANESDIRKLEAAADVGNKIDFNFIATMNMNTEKEDHLMAAFMFDINDSGYITI 488
QY 422 DELQACTEFGCLD-TPLDDMIKEIDLNDGKIDFSEFTAMWRKGD-GVGRSRTMMK 476
DB 489 DELQAEKMGMDGPETIQIIEIVTDNDGRIDYDEFVAMWRKGNPGAENGTTVKNK 545
RESULT 13
AAG31159
ID AAG31159 standard; Protein; 408 AA.

XX AC AG31159;
XX AC 17-OCT-2000 (first entry)
XX DT Arabidopsis thaliana protein fragment SEQ ID NO: 37373.
XX DE
XX KW Protein identification; signal transduction pathway; metabolic pathway;
XX KW hybridisation assay; Genetic mapping; gene expression control; promoter;
XX KW termination sequence.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX XX
XX PD 06-SEP-2000.
XX PF
XX PF 25-FEB-2000; 2000EP-0301439.
XX XX
XX PR 25-FEB-1999; 99US-0121825.
XX PR 05-MAR-1999; 99US-0123180.
XX PR 09-MAR-1999; 99US-0123548.
XX PR 23-MAR-1999; 99US-0125788.
XX PR 25-MAR-1999; 99US-0126264.
XX PR 29-MAR-1999; 99US-0126785.
XX PR 01-APR-1999; 99US-0127462.
XX PR 06-APR-1999; 99US-0128234.
XX PR 08-APR-1999; 99US-0128714.
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XX PR 05-MAY-1999; 99US-0132485.
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XX PR 20-MAY-1999; 99US-0135124.
XX PR 21-MAY-1999; 99US-0135353.
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XX PR 25-MAY-1999; 99US-0136021.
XX PR 27-MAY-1999; 99US-0136392.
XX PR 28-MAY-1999; 99US-0136782.
XX PR 01-JUN-1999; 99US-0137222.
XX PR 03-JUN-1999; 99US-0137528.
XX PR 04-JUN-1999; 99US-0137502.
XX PR 07-JUN-1999; 99US-0137724.
XX PR 08-JUN-1999; 99US-0138094.
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XX PR 01-JUL-1999; 99US-0142154.
XX PR 02-JUL-1999; 99US-0142055.
XX PR 06-JUL-1999; 99US-0142390.
XX PR 08-JUL-1999; 99US-0142803.
XX PR 09-JUL-1999; 99US-0142920.
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XX PR 19-JUL-1999; 99US-0144332.
XX PR 19-JUL-1999; 99US-0144333.
XX PR 19-JUL-1999; 99US-0144334.
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XX PR 20-JUL-1999; 99US-0144884.
XX PR 21-JUL-1999; 99US-0144814.
XX PR 21-JUL-1999; 99US-0145086.
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XX PR 23-JUL-1999; 99US-0145145.
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XX PR 26-JUL-1999; 99US-0145276.
XX PR 27-JUL-1999; 99US-0145913.
XX PR 27-JUL-1999; 99US-0145918.
XX PR 27-JUL-1999; 99US-0145919.
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XX PR 10-AUG-1999; 99US-0148171.
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XX PR 18-AUG-1999; 99US-0149425.
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XX PR 20-AUG-1999; 99US-0149723.
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XX PR 23-AUG-1999; 99US-0149902.
XX PR 23-AUG-1999; 99US-0149930.

PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151343.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
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PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 23-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
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PR 14-OCT-1999; 99US-0159329.
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PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 58.2%; Score 1509; DB 21; Length 408;

Best Local Similarity 69.4%; Pred. No. 7,le=126;

Matches 284; Conservative 56; Mismatches 67; Indels 2; Gaps 2;

QY 78 MHHLSEHNVVRIKGTEDSVFVHVMVEVCEGGELEFDRIVSKGHFSEBAVKLIKTLGV 137
DB 1 MHHLAGHSIVTIKGAEDSLYVHVMELCAGGELFDRITQRGHYSERKAAELTKIIVG 60
QY 138 VEACHSLGVHMRDLKPENFLFDSPKDAKUKATDFGLSVFYKPGQVLYDVVGSPPYVAPE 197
DB 61 VEACHSLGVHMRDLKPENFLVNVKDDDFSLKAITDGLSVFFKPGQIFTDVWGSPPYVAPE 120
QY 198 VLKCYGPEIDVWAGVLYTLVLSGVPFPAETESGIFROILQGLDFKSDPWPPTISEAA 257
DB 121 VLLKRYGPEADVWAGVLYTLVLSGVPFPAETESGIFROILQGLDFKSDPWPPTISEAA 180
QY 258 KDLTYKMLERSPKKRISSAEALCHPWIDFQAAPEKPLDPVLSRLKQFSQMNKIKMAL 217
DB 181 KDLTYKMLERSPKKRISSAEALCHPWIDFQAAPEKPLDPVLSRLKQFSQMNKIKMAL 240

QY 318 RVIAERLSEEEIGGLKELFKMIDTNSQITTFEELKAGLRKVGSELMESEIKSLMDAADI 377
DB 241 KVIASLSEEEIAGLRKEMFQAMDTONGAITFDELKAGLRKVGSTLKDTEIHDLMDAADV 300
QY 378 DNSGTIDYGEFLAATLHNKMRERELVAAFSDFDKDGSYITIDELQSACTEGLCDTP 437
DB 301 DNSGTIDYSEFTAAATHLNKLREERELVAAFOYFDKDGSGFITIDELQQACVERGMADV 360
QY 438 LDMIKELIDLDNDGKIDFSEFTAMMRKGD-GVGRSRTMMKNLNFNIADA 485
DB 361 LEDIIEVDQNDGKIDYGEFVEMMQKNAGVGR-RTWRNSLNISMRA 408
RESULT 14
AAG46565
ID AAG46565 standard; Protein; 463 AA.
XX
AC AAG46565;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 58596.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
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PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
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PR 04-MAY-1999; 99US-0132407.
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PR 06-MAY-1999; 99US-0132485.
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PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.

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PR 08-JUN-1999;	99US-0138094.	PR 09-AUG-1999;	99US-0147493.
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PR 16-JUN-1999;	99US-0139452.	PR 12-AUG-1999;	99US-0148341.
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PR 17-JUN-1999;	99US-0139492.	PR 13-AUG-1999;	99US-0148684.
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PR 18-JUN-1999;	99US-0139763.	PR 27-AUG-1999;	99US-0151066.
PR 21-JUN-1999;	99US-0139817.	PR 27-AUG-1999;	99US-0151080.
PR 22-JUN-1999;	99US-0139899.	PR 30-AUG-1999;	99US-0151303.
PR 23-JUN-1999;	99US-0140353.	PR 31-AUG-1999;	99US-0151438.
PR 23-JUN-1999;	99US-0140354.	PR 01-SEP-1999;	99US-0151930.
PR 24-JUN-1999;	99US-0140695.	PR 07-SEP-1999;	99US-0152363.
PR 28-JUN-1999;	99US-0140823.	PR 10-SEP-1999;	99US-0152363.
PR 29-JUN-1999;	99US-0140991.	PR 13-SEP-1999;	99US-0153070.
PR 30-JUN-1999;	99US-0141287.	PR 15-SEP-1999;	99US-0153758.
PR 01-JUL-1999;	99US-0141842.	PR 16-SEP-1999;	99US-0154018.
PR 01-JUL-1999;	99US-0142154.	PR 20-SEP-1999;	99US-0154039.
PR 02-JUL-1999;	99US-0142055.	PR 22-SEP-1999;	99US-0154779.
PR 06-JUL-1999;	99US-0142390.	PR 23-SEP-1999;	99US-0155139.
PR 08-JUL-1999;	99US-0142803.	PR 24-SEP-1999;	99US-0155486.
PR 09-JUL-1999;	99US-0142920.	PR 28-SEP-1999;	99US-0155659.
PR 12-JUL-1999;	99US-0143542.	PR 29-SEP-1999;	99US-0156458.
PR 13-JUL-1999;	99US-0143542.	PR 04-OCT-1999;	99US-0156596.
PR 15-JUL-1999;	99US-0143524.	PR 05-OCT-1999;	99US-0157117.
PR 15-JUL-1999;	99US-0144005.	PR 06-OCT-1999;	99US-0157753.
PR 16-JUL-1999;	99US-0144085.	PR 07-OCT-1999;	99US-0157865.
PR 16-JUL-1999;	99US-0144086.	PR 08-OCT-1999;	99US-0158029.
PR 19-JUL-1999;	99US-0144325.	PR 12-OCT-1999;	99US-0158232.
PR 19-JUL-1999;	99US-0144331.	PR 13-OCT-1999;	99US-0158369.
PR 19-JUL-1999;	99US-0144332.	PR 13-OCT-1999;	99US-0159293.
PR 19-JUL-1999;	99US-0144333.	PR 13-OCT-1999;	99US-0159294.
PR 19-JUL-1999;	99US-0144334.	PR 14-OCT-1999;	99US-0159295.
PR 19-JUL-1999;	99US-0144335.	PR 14-OCT-1999;	99US-0159329.
PR 20-JUL-1999;	99US-0144352.	PR 14-OCT-1999;	99US-0159330.
PR 20-JUL-1999;	99US-0144352.	PR 14-OCT-1999;	99US-0159331.
PR 21-JUL-1999;	99US-0144884.	PR 14-OCT-1999;	99US-0159367.
PR 21-JUL-1999;	99US-0144814.	PR 18-OCT-1999;	99US-0159638.
PR 21-JUL-1999;	99US-0145086.	PR 21-OCT-1999;	99US-0159684.
PR 21-JUL-1999;	99US-0145088.	PR 21-OCT-1999;	99US-0160741.
PR 22-JUL-1999;	99US-0145085.	PR 21-OCT-1999;	99US-0160767.
PR 22-JUL-1999;	99US-0145087.	PR 21-OCT-1999;	99US-0160768.
PR 22-JUL-1999;	99US-0145089.	PR 21-OCT-1999;	99US-0160770.
PR 22-JUL-1999;	99US-0145192.	PR 21-OCT-1999;	99US-0160814.
PR 23-JUL-1999;	99US-0145145.	PR 22-OCT-1999;	99US-0160815.
PR 23-JUL-1999;	99US-0145218.	PR 22-OCT-1999;	99US-0160980.
PR 23-JUL-1999;	99US-0145224.	PR 22-OCT-1999;	99US-0160981.
PR 26-JUL-1999;	99US-0145276.	PR 25-OCT-1999;	99US-0160989.
PR 27-JUL-1999;	99US-0145313.	PR 25-OCT-1999;	99US-0161404.
PR 27-JUL-1999;	99US-0145318.	PR 25-OCT-1999;	99US-0161405.
PR 27-JUL-1999;	99US-0145919.	PR 26-OCT-1999;	99US-0161359.
PR 28-JUL-1999;	99US-0145951.	PR 26-OCT-1999;	99US-0161360.
PR 02-AUG-1999;	99US-0146386.	PR 28-OCT-1999;	99US-0161361.
PR 02-AUG-1999;	99US-0146388.	PR 28-OCT-1999;	99US-0161920.
PR 02-AUG-1999;	99US-0146389.	PR 28-OCT-1999;	99US-0161992.
PR 03-AUG-1999;	99US-0147038.	PR 28-OCT-1999;	99US-0161993.
PR 04-AUG-1999;	99US-0147204.	PR 29-OCT-1999;	99US-0162142.
PR 05-AUG-1999;	99US-0147302.		
PR 05-AUG-1999;	99US-0147192.		
PR 05-AUG-1999;	99US-0147260.		

Query Match 57.9%; Score 1501; DB 21; Length 463;
 Best Local Similarity 61.4%; Pred. No. 4.4e-135;

Matches 281; Conservative 79; Mismatches 92; Indels 6; Gaps 3;
QY 26 YLLGKLGQGGFTTYLCTEKSTSANVACKSIPKRVLCREYEDVWREIQIMHLSHP 85
DB 8 YSLGKLGQGGFTTYLCTEKSTSANVACKSIPKRVLCREYEDVWREIQIMHLSHP 67
QY 86 NVVRKIGTYEDSVFVHVMVECEGELFDRIVSKGHFSEREAVKLIKILGVVEACHSLG 145
DB 68 NVEIKGAYEDKSHVHVMVECEGELFDRIVSKGHFSEREAVKLIKILGVVEACHSLG 127
QY 146 VMHRLKPNELFDSPKDDAKLKTDFGLSVFYKPGQYLYDVVSGPYVVAPEVLKCYGP 205
DB 128 VTHRLKPNELFDSPKDDAKLKTDFGLSVFYKPGQYLYDVVSGPYVVAPEVLKCYGP 187
QY 206 EIDVNSAGVILVLLSGVPPWAEETSGIFRQILQGLDKPDKSPWPTISAAKDLIVKML 265
DB 188 EADVNSAGVILVLLSGVPPWAEETSGIFRQILQGLDKPDKSPWPTISAAKDLIVKML 247
QY 266 ERSKPKRISAHEALCHPWIVDEQAAPDLPAVLRLKQFSQNMKKIKMALRVIAERLS 325
DB 248 NSDPKQRLTAAGVLAHPWIKEDGEAPDVLNNAVMSRLKQFKAMNFKVALRVIAERLS 307
QY 326 EREIGGLKELFKMIDTNSGTTTPEELKAGLKVYGSSELMSESEIKSLMDADIDNSGTIDY 385
DB 308 EBEIIGLKEFMFGMDTDSGTTTPEELKAGLKVYGSSELMSESEIKSLMDADIDNSGTIDY 367
QY 386 GEFLAATLHNMKWEREEILVAAFSDFDKDGSYITIDELQSACTEFLGCD-TPLDMMIKE 444
DB 368 GFETATWHINLDRHEELHLYSAFHFDKNSGYITMELEQALREFGNDRDIKEIIE 427
QY 445 IOLDNDGKIDFSEFTAMRKQ--DVGGRSRWTKMLNF 480
DB 428 VDGNDGRINYDEFVAMVRKGNPDPIPKR---RELSP 462

RESULT 15
AAG65758
ID AAG65758 standard; Protein; 280 AA.
AC AAG65758;
DT 07-JAN-2002 (first entry)
DE ATCDPK2 kinase domain sequence.
XX Plant protoplast; gene expression; Arabidopsis; PK; CDPK; ATCDPK2;
KW calcium activated protein kinase; calcium dependant protein kinase.
XX Arabidopsis thaliana.
XX WO200168920-A1.
XX 20-SEP-2001.
XX 13-MAR-2001; 2001WO-US07999.
XX 13-MAR-2000; 2000US-189074P.
PA (GENO) GEN HOSPITAL CORP.
PI Sheen J;
XX WPI; 2001-611395/70.
PT Using plant protoplast expression systems for rapidly screening
PT libraries of nucleic acids to identify gene that modulate expression of
PT target genes -
XX Examples; Fig 3B; 95pp; English.
XX The invention provides a high through-put assay for rapidly screening
CC a library of nucleic acid molecules to identify a gene product that
CC modulates expression of a gene of interest in plant protoplasts. The

method comprises: (1) introducing into 1 or more plant protoplasts:
(a) a reporter gene construct operably linked to a promoter of a gene of
interest; and (b) a member of a library of nucleic acid molecules (the
library member is expressed in the plant protoplasts); and (2) screening
the protoplasts to determine whether the amount of gene expression of the
reporter gene construct changes in response to the expression of the
library members, a change in gene expression of the reporter gene
construct identifying the gene product expressed by the library member as
1 that modulates expression of the gene of interest. The present sequence
represents the amino acid sequence of Arabidopsis calcium dependant
protein kinase (CDPK) ATCDPK2 kinase domain.
SQ Sequence 280 AA;
Query Match 57.8%; Score 1500; DB 22; Length 280;
Best Local Similarity 100.0%; Pred. No. 2.6e-125;
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 PSNTVLPYQTPRLRDHYLLGKLGQGGFTTYLCTEKSTSANVACKSIPKRVLCREYDYE 69
DB 1 PSNTVLPYQTPRLRDHYLLGKLGQGGFTTYLCTEKSTSANVACKSIPKRVLCREYDYE 60
QY 70 DVWREIQIMHLSHPNVVRKIGTYEDSVFVHVMVECEGELFDRIVSKGHFSEREAVK 129
DB 61 DVWREIQIMHLSHPNVVRKIGTYEDSVFVHVMVECEGELFDRIVSKGHFSEREAVK 120
QY 130 LIKTILGVVEACHSLGVHMRDLKPNELFDSPKDDAKLKTDFGLSVFYKPGQYLYDVVVG 189
DB 121 LIKTILGVVEACHSLGVHMRDLKPNELFDSPKDDAKLKTDFGLSVFYKPGQYLYDVVVG 180
QY 190 SPYVVAPEVLKCYGPEDVMSAGVILVLLSGVPPWAEETSGIFRQILQGLDKPDKSDP 249
DB 181 SPYVVAPEVLKCYGPEDVMSAGVILVLLSGVPPWAEETSGIFRQILQGLDKPDKSDP 240
QY 250 WPTISEAAKDLIYKMLERSPKKRISAHEALCHPWIVDEQA 289
DB 241 WPTISEAAKDLIYKMLERSPKKRISAHEALCHPWIVDEQA 280

Search completed: February 13, 2003, 21:09:11
Job time : 62 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 13, 2003, 21:08:08 ; Search time 22 Seconds
(without alignments)

662.016 Million cell updates/sec

Title: US-09-848-806-1

Perfect score: 2593

Sequence: 1 METKENRRPSNTVLPYQTP.....KMLNFNIADAFVDGKSD 495

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 2942292 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/prodata/2/aa/5A_COMB.pep.*
- 2: /cgn2_6/prodata/2/aa/5B_COMB.pep.*
- 3: /cgn2_6/prodata/2/aa/6A_COMB.pep.*
- 4: /cgn2_6/prodata/2/aa/6B_COMB.pep.*
- 5: /cgn2_6/prodata/2/aa/PCTUS_COMB.pep.*
- 6: /cgn2_6/prodata/2/aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1927	74.3	463	1	US-07-951-715A-25
2	1927	74.3	463	2	US-08-459-448A-25
3	1927	74.3	463	3	US-08-459-595A-25
4	1927	74.3	463	3	US-08-459-504B-25
5	1927	74.3	463	3	US-08-459-444-25
6	1927	74.3	463	4	US-09-547-422-25
7	1672.5	64.5	639	4	US-09-347-801-17
8	1437.5	55.4	464	1	US-07-951-715A-22
9	1437.5	55.4	464	2	US-08-459-448A-22
10	1437.5	55.4	464	3	US-08-459-595A-22
11	1437.5	55.4	464	3	US-08-459-504B-22
12	1437.5	55.4	464	3	US-08-459-444-22
13	1437.5	55.4	464	4	US-09-547-422-22
14	1277.5	49.3	408	1	US-07-951-715A-21
15	1277.5	49.3	408	2	US-08-459-448A-21
16	1277.5	49.3	408	3	US-08-459-595A-21
17	1277.5	49.3	408	3	US-08-459-504B-21
18	1277.5	49.3	408	3	US-08-459-444-21
19	1277.5	49.3	408	4	US-09-547-422-21
20	829	32.0	623	4	US-09-347-801-4
21	826	31.9	625	4	US-09-347-801-18
22	800	30.9	576	4	US-09-347-801-19
23	771.5	29.8	456	1	US-08-464-164-2
24	771.5	29.8	456	1	US-08-338-057-2
25	771.5	29.8	456	2	US-08-468-416-2
26	622	24.0	520	4	US-09-357-825B-20
27	587.5	22.7	370	2	US-08-878-989-19

28	587.5	22.7	370	4	US-09-372-796-19
29	587.5	22.7	370	4	US-09-457-040B-31
30	582	22.4	517	4	US-09-357-825B-21
31	548	21.1	264	2	US-07-857-224B-19
32	543.5	21.0	556	4	US-09-800-960-4
33	539	20.8	565	4	US-09-800-960-2
34	538	20.7	264	2	US-07-857-224B-18
35	535.5	20.7	424	2	US-08-715-568A-1
36	533.5	20.6	387	1	US-08-713-828-3
37	533.5	20.6	387	2	US-08-919-627-3
38	533.5	20.6	387	2	US-09-096-245-3
39	533.5	20.6	387	4	US-09-457-040B-30
40	532.5	20.5	343	2	US-08-878-989-5
41	532.5	20.5	343	2	US-09-272-796-5
42	530	20.4	295	1	US-07-951-715A-23
43	530	20.4	295	2	US-08-459-448A-23
44	530	20.4	295	3	US-08-459-595A-23
45	530	20.4	295	3	US-08-459-504B-23

ALIGNMENTS

RESULT 1
US-07-951-715A-25
; Sequence 25, Application US/07951715A
; Patent No. 5625136

GENERAL INFORMATION:

APPLICANT: Koziel, Michael G.
APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Launis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
INSECTICIDAL ACTIVITY IN MAIZE

NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/951,715A
FILING DATE: 25-SEP-1992
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8615
TELEFAX: (919)541-8689

INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:
LENGTH: 463 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FEATURE:

NAME/KEY: Protein

LOCATION: 1..463

OTHER INFORMATION: /note= "protein sequence for

OTHER INFORMATION: soybean CDPK as shown in Figure 34."

US-07-951-715A-25

Query Match 74.3%; Score 1927; DB 1; Length 463;

Best Local Similarity 78.7%; Pred. No. 1e-152;

Matches 365; Conservative 49; Mismatches 48; Indels 2; Gaps 2;

14 VLPYOTPLRDLHYLLGKLGOGFGTTTLCTEKSTSNANYACKSIKPKLVCRDVEDYVWR 73

1 VLPQSTQNIREVVEVGRKLGOGFGTTTCTRASGKFKACKSIKPKLLCKEDYEDVWR 60

74 BQIMHHLSEHPNVRIKGYEDSVFVHIVMEVCEGELFDRIVSKGHFSREAVKLTKT 133

61 BQIMHHLSEHPNVRIKGYEDSVFVHIVMEVCEGELFDRIVSKGHFSREAVKLTKT 120

134 ILGVVEACHSLGVNHRDLKPNELFSPKDDAKLKATDFGLSVFYKPGQYLYDVVGSPPY 193

121 IVEVVEACHSLGVNHRDLKPNELFSPKDDAKLKATDFGLSVFYKPGQYLYDVVGSPPY 180

194 VAPVLLKCVGPEIDVWSAGVILYLLSGVPPFWAETESGIFRQILQKLFDPKDPWPTI 253

181 VAPEVLRKLVGPEIDVWSAGVILYLLSGVPPFWAETESGIFRQILQKLFDPKDPWPTI 240

254 SEAAKLIYKMLERSPKKRIISAHEALCHPWIVDEQAAPKPLDPAVLRLKQFSOMNKK 313

241 SDSAKDLIRKMLDONKTRTLTAHEVLRHPWVDNIAAPKPLDSAVLSRLKQFSAMNKLK 300

314 KQALRVIAERLSEBEEIGGLKELPKMTDNTSGTIIPFELKAGLKRVGSELMSEIKSLMD 373

301 KQALRVIAERLSEBEEIGGLKELPKMTDNTSGTIIPFELKAGLKRVGSELMSEIKSLMD 360

374 AADIDNSGTIDYGEFFLAATLHMNMKREELIVAAFDKDGSGVITIDELQSACTEFL 433

361 AADIDKSGTIDYGEFFLAATVHLNKLREELIVAAFDKDGSGVITIDELQSACTEFL 420

434 CDTPLDMIXEIDLNDCKIDPSEFTAMRKGD-GVGRSRTWKK 476

421 DDHIDDMIXEIDLNDCKIDPSEFTAMRKGD-GVGRSRTWKK 463

RESULT 2

US-08-459-448A-25

Sequence 25, Application US/08459448A

Patent No. 5853336

GENERAL INFORMATION:

APPLICANT: Koziel, Michael G.

APPLICANT: Desai, Nalini M.

APPLICANT: Lewis, Kelly S.

APPLICANT: Kramer, Vance C.

APPLICANT: Warren, Gregory W.

APPLICANT: Evola, Stephen V.

APPLICANT: Crossland, Lyle D.

APPLICANT: Wright, Martha S.

APPLICANT: Merlin, Ellis J.

APPLICANT: Launis, Karen L.

APPLICANT: Rothstein, Steven J.

APPLICANT: Bowman, Cindy G.

APPLICANT: Dawson, John L.

APPLICANT: Dunder, Erik M.

APPLICANT: Pace, Gary M.

APPLICANT: Suttie, Janet L.

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED

TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 589336artis Corporation

STREET: Patent & Trademark Dept., 520 White Plains

CITY: Tarrytown

STATE: New York

COUNTRY: USA

ZIP: 10591-9005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/459,448A

FILING DATE: 02-JUN-1995

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/951,715

FILING DATE: 25-SEP-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/772,027

FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: Pace, Gary M.

REGISTRATION NUMBER: 40403

REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919)541-8582

TELEFAX: (919)541-8689

INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:

LENGTH: 463 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

FEATURE:

NAME/KEY: Protein

LOCATION: 1..463

OTHER INFORMATION: /note= "protein sequence for

OTHER INFORMATION: soybean CDPK as shown in Figure 34."

US-08-459-448A-25

Query Match 74.3%; Score 1927; DB 2; Length 463;

Best Local Similarity 78.7%; Pred. No. 1e-152;

Matches 365; Conservative 49; Mismatches 48; Indels 2; Gaps 2;

14 VLPYOTPLRDLHYLLGKLGOGFGTTTLCTEKSTSNANYACKSIKPKLVCRDVEDYVWR 73

1 VLPQSTQNIREVVEVGRKLGOGFGTTTCTRASGKFKACKSIKPKLLCKEDYEDVWR 60

74 BQIMHHLSEHPNVRIKGYEDSVFVHIVMEVCEGELFDRIVSKGHFSREAVKLTKT 133

61 BQIMHHLSEHPNVRIKGYEDSVFVHIVMEVCEGELFDRIVSKGHFSREAVKLTKT 120

134 ILGVVEACHSLGVNHRDLKPNELFSPKDDAKLKATDFGLSVFYKPGQYLYDVVGSPPY 193

121 IVEVVEACHSLGVNHRDLKPNELFSPKDDAKLKATDFGLSVFYKPGQYLYDVVGSPPY 180

194 VAPVLLKCVGPEIDVWSAGVILYLLSGVPPFWAETESGIFRQILQKLFDPKDPWPTI 253

181 VAPEVLRKLVGPEIDVWSAGVILYLLSGVPPFWAETESGIFRQILQKLFDPKDPWPTI 240

254 SEAAKLIYKMLERSPKKRIISAHEALCHPWIVDEQAAPKPLDPAVLRLKQFSOMNKK 313

241 SDSAKDLIRKMLDONKTRTLTAHEVLRHPWVDNIAAPKPLDSAVLSRLKQFSAMNKLK 300

314 KQALRVIAERLSEBEEIGGLKELPKMTDNTSGTIIPFELKAGLKRVGSELMSEIKSLMD 373

Db 301 KVALVIAERLSEIEIGGLKELFKXMDITDNGSTITFDELKQGLKRVGSELMSEIKDLMD 360
QY 374 AADINSGTIDYGEFLAATLHMNWEREELVAAFSDFDKDGGYITIDELQSACTEFG 433
Db 361 AADIDKSGTIDYGEFLAATVHLNLEREENLVSAFSDKDDGGYITIDELQSACTEFG 420
QY 434 CDTPLDDMIKEIDLNDGKIDFSEPTAMRKGD-GVGRSRTMVK 476
Db 421 DDHIDDMIKEIDLNDGQIDYGEFAAMVRKNGGIGR-RTMRK 463

RESULT 3
US-08-459-595A-25
Sequence 25, Application US/08459595A
Patent No. 6018104
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Launis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSER: No. 6018104artis Corporation
STREET: Patent & Trademark Dept., 520 White Plains
CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591-9005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,595A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: 40403
REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8582
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 463 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

HYPOTHETICAL: NO
FEATURE:
NAME/KEY: Protein
LOCATION: 1..463
OTHER INFORMATION: /note= "protein sequence for
OTHER INFORMATION: soybean CDPK as shown in Figure 34."
US-08-459-595A-25
Query Match 74.3%; Score 1927; DB 3; Length 463;
Best Local Similarity 78.7%; Pred. No. 1e-152;
Matches 365; Conservative 49; Mismatches 48; Indels 2; Gaps 2;
QY 14 VLPYQTPRLRDHYLLGKLGOGFGTTTLCETKSTANVACKSIPKRLKLVCRDEYEDVNR 73
Db 1 VLPQRTQVIREVYVGRKLGOGFGTTFCTRRASGCKPACKSIPKRLKLVCRDEYEDVNR 60
QY 74 EIQIMHLSHPNVVRIKGTYESVFIHVMVECEGELFDRIVSKGHFSEREAVKLIKT 133
Db 61 EIQIMHLSHPNVVRIKGTYESVFIHVMVECEGELFDRIVSKGHFSEREAVKLIKT 120
QY 134 ILGVVEACHSLGVNHRDLKPNFLFDSKDDAKLKATDFGLSVFYKPGQVLYDVVGSPPY 193
Db 121 IVEVVEACHSLGVNHRDLKPNFLFDTDEDAKLKATDFGLSVFYKPGSFCDVVGSPY 180
QY 194 VAPEVLKKCYGPEIDVMSAGVILYLLSGVPPFWAETESGIFQILQGLDKFSDPMTI 253
Db 181 VAPEVLKLYGPESDVMSAGVILYLLSGVPPFWAETESGIFQILQGLDKFSDPMTI 240
QY 254 SEAAKDLIYKMLERSPKRISAHEALCHPWIVDEQAAPDKPLDPAVLRLKQFSQNNKIK 313
Db 241 SDSAKDLIRKMLDQNPXTRLTAEVLRHPWIVDNPATAPDKPLDSAVLSRLKQFSQNNKIK 300
QY 314 KVALVIAERLSEIEIGGLKELFKXMDITDNGSTITFDELKQGLKRVGSELMSEIKSLMD 373
Db 301 KVALVIAERLSEIEIGGLKELFKXMDITDNGSTITFDELKQGLKRVGSELMSEIKDLMD 360
QY 374 AADINSGTIDYGEFLAATLHMNWEREELVAAFSDFDKDGGYITIDELQSACTEFG 433
Db 361 AADIDKSGTIDYGEFLAATVHLNLEREENLVSAFSDKDDGGYITIDELQSACTEFG 420
QY 434 CDTPLDDMIKEIDLNDGKIDFSEPTAMRKGD-GVGRSRTMVK 476
Db 421 DDHIDDMIKEIDLNDGQIDYGEFAAMVRKNGGIGR-RTMRK 463

RESULT 4
US-08-459-504B-25
Sequence 25, Application US/08459504B
Patent No. 6075185
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Launis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSER: No. 6075185artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park

QY 434 CDTPLDDMIKEIDLDNCKIDFSEFTAMMRKGD-GVGRSRTMMK 476
DB 421 DDHIDDMIKEDQNDQGDIDYGEFAAMRRNGGIGR-RTMRK 463

RESULT 5
US-08-459-444-25
Sequence 0, Application US/08459444
Patent No. 6121014
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Lauis, Karen L.
TITLE OF INVENTION: METHOD FOR PRODUCING A PLANT-OPTIMIZED
NUCLEIC ACID CODING SEQUENCE

NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6121014artis Agribusiness Biotechnology Research, Inc.
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,444A
FILING DATE: 02-Jun-1995
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-18805/PL/CGC1577/CIP/DIV6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: soybean CDPK as shown in Figure 34."

SEQUENCE CHARACTERISTICS:
LENGTH: 463 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: Protein
LOCATION: 1..463
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-08-459-444-25

Query Match 74.3%; Score 1927; DB 3; Length 463;
Best Local Similarity 78.7%; Pred. No. 1e-152;
Matches 365; Conservative 49; Mismatches 48; Indels 2; Gaps 2;

QY 14 VLPYOTPLRHHLLGKLGQGGTGTTLCTEKTSTANYACKSIPKELVCREDYEDVNR 73
DB 1 VLPQFTQNIREVVEVGRKLGQGGTGTTECTRRASGGKGFACKSIPKELCKEDYEDVNR 60

QY 74 ETQIMHLSHPNVRIKGTIEDSVFVHIVMEVCEGGELFDRIVSKGHPSEAEVLIKT 133
DB 61 ETQIMHLSHANVRIEGTYEDSTAVELVNLCEGGELEFDRIVQKHYSERQAALIKT 120

QY 134 ILGVVEACHSLGVHMDLKPENFLPDSKDKALKATDFGLSVFYKPGQYLYDVVGSPPY 193
DB 121 IVEVVEACHSLGVHMDLKPENFLDTEDEAKALKATDFGLSVFYKPGSEFCDVVGSPPY 180

QY 194 VAPEVLKCYGPEIDVWAGVILYLLSGVPPFWAESPFGIIRLOLQKLDKFSKDPPTI 253
DB 181 VAPEVLKLYGPESDVWAGVILYLLSGVPPFWAESPFGIIRLOLQKLDKFSKDPPTI 240

QY 254 SEAAKDLIVKMLERSPKRISAEHALCHPWVDEQAAPDKLPDPAVLSRLKQFSQMNKIK 313
DB 241 SUSAKDLIRKMLDQPKRLTAHEVLRHPWVDNIAEPKPLDSAVLSRLKQFSQMNKIK 300

QY 314 KVALRVIAERLSEEEIGGLKELFKMIDTNSGTTTFPELKGKRVGSELMESEIKLMD 373
DB 301 KVALRVIAERLSEEEIGGLKELFKMIDTNSGTTTFPELKGKRVGSELMESEIKLMD 360

QY 374 AADIDNSGTDYGEFLAATLHNKWEREILVAAPSDFDKSGSVITIDELQSACTEFGLE 433
DB 361 AADIDKSGTIDYGEFLAATLHNKWEREILVAAPSDFDKSGSVITIDELQSACTEFGLE 420

US-08-459-504B-25
Query Match 74.3%; Score 1927; DB 3; Length 463;
Best Local Similarity 78.7%; Pred. No. 1e-152;
Matches 365; Conservative 49; Mismatches 48; Indels 2; Gaps 2;

QY 14 VLPYOTPLRHHLLGKLGQGGTGTTLCTEKTSTANYACKSIPKELVCREDYEDVNR 73
DB 1 VLPQFTQNIREVVEVGRKLGQGGTGTTECTRRASGGKGFACKSIPKELCKEDYEDVNR 60

QY 74 ETQIMHLSHPNVRIKGTIEDSVFVHIVMEVCEGGELFDRIVSKGHPSEAEVLIKT 133
DB 61 ETQIMHLSHANVRIEGTYEDSTAVELVNLCEGGELEFDRIVQKHYSERQAALIKT 120

QY 134 ILGVVEACHSLGVHMDLKPENFLPDSKDKALKATDFGLSVFYKPGQYLYDVVGSPPY 193
DB 121 IVEVVEACHSLGVHMDLKPENFLDTEDEAKALKATDFGLSVFYKPGSEFCDVVGSPPY 180

QY 194 VAPEVLKCYGPEIDVWAGVILYLLSGVPPFWAESPFGIIRLOLQKLDKFSKDPPTI 253
DB 181 VAPEVLKLYGPESDVWAGVILYLLSGVPPFWAESPFGIIRLOLQKLDKFSKDPPTI 240

QY 254 SEAAKDLIVKMLERSPKRISAEHALCHPWVDEQAAPDKLPDPAVLSRLKQFSQMNKIK 313
DB 241 SUSAKDLIRKMLDQPKRLTAHEVLRHPWVDNIAEPKPLDSAVLSRLKQFSQMNKIK 300

QY 314 KVALRVIAERLSEEEIGGLKELFKMIDTNSGTTTFPELKGKRVGSELMESEIKLMD 373
DB 301 KVALRVIAERLSEEEIGGLKELFKMIDTNSGTTTFPELKGKRVGSELMESEIKLMD 360

QY 374 AADIDNSGTDYGEFLAATLHNKWEREILVAAPSDFDKSGSVITIDELQSACTEFGLE 433
DB 361 AADIDKSGTIDYGEFLAATLHNKWEREILVAAPSDFDKSGSVITIDELQSACTEFGLE 420

Db 1 VLPQRTQNTREVYEVGRKLGQGGQGGTTFCTTRASGGKFAKSPKRLKLLCKEDYEDVWR 60
QY 74 EIQIMHHLSEHNVRIRKTYEDSVFVHVMVCEGGELFDRIVSKGHFSREAVKIKT 133
Db 61 EIQIMHHLSEHANVRIEGTYEDSTAVHLVWMLCEGGELFDRIVQKHYSERQARLIKT 120
QY 134 ILGVWACHSLGVMHRDLKPNFLDPSKDDAKLKATDFGLSVFYKPGCYLYDVVVGSPYY 193
Db 121 IVEVWACHSLGVMHRDLKPNFLDFTIDEDAKLKATDFGLSVFYKPGESCDVVVGSPYY 180
QY 194 VAEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETSGIFRQILQKLDKDFKSDPWPPTI 253
Db 181 VAEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETSGIFRQILQKLDKDFHSEPPWPSI 240
QY 254 SEAKDLIVKMLERSPKKISAEALCHPWIVDEQAAPDKPLDPAVLRLKQFQFOMNKK 313
Db 241 SDSAKDLIRKMLDQNPKRLTAHEVLRHPWIVDDNIAPDKPLDSAVLSRLKQFSAWNLK 300
QY 314 KVALRVIARLSSEEEIGGLKELFKMIDTNSGTTTFEELKAGLKVGSSELMESEIKSLMD 373
Db 301 KVALRVIARLSSEEEIGGLKELFKMIDTNSGTTTFEELKAGLKVGSSELMESEIKSLMD 360
QY 374 AADIDNSGTTIDYGEFLAATLHNKMERREILVAAPSDFDKDGSGYITIDELQSACTEFL 433
Db 361 AADIDNSGTTIDYGEFLAATVHLNKLREENTLSAFSYFDKDGSGYITIDELQSACTEFL 420
QY 434 CDTPLDDMIKEIDLNDGKIDFSEFTAMRKGD-GVGRSRTMMK 476
Db 421 DDTHIDDMIKEDQNDGQIDYGEFAAMRKNGGIGR-RTMRK 463

RESULT 6

US-09-547-422-25
; Sequence 0, Application US/09547422
; Patent No. 6320100
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; Desai, Nalini M.
; Lewis, Kelly S.
; Kramer, Vance C.
; Warren, Gregory W.
; Evola, Stephen V.
; Crossland, Lyle D.
; Wright, Martha S.
; Merlin, Ellis J.
; Lounis, Karen L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6320100artis Agribusiness Biotechnology Research, Inc.
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/547,422
; FILING DATE: 11-Apr-2000
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/459,595
; FILING DATE: 02-JUN-1995
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:

; NAME: Weigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: S-18805H
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8587
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: /note= "protein sequence for
; soybean CDPK as shown in Figure 34."
; SEQUENCE CHARACTERISTICS:
; LENGTH: 463 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..463
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-547-422-25

Query Match 74.3%; Score 1927; DB 4; Length 463;
Best Local Similarity 78.7%; Pred. No. 1e-152;
Matches 365; Conservative 49; Mismatches 48; Indels 2; Gaps 2;
QY 14 VLPYQTPRLRHYLLGKLGQGGQGGTTFCTTRASGGKFAKSPKRLKLLCKEDYEDVWR 73
Db 1 VLPQRTQNTREVYEVGRKLGQGGQGGTTFCTTRASGGKFAKSPKRLKLLCKEDYEDVWR 60
QY 74 EIQIMHHLSEHNVRIRKTYEDSVFVHVMVCEGGELFDRIVSKGHFSREAVKIKT 133
Db 61 EIQIMHHLSEHANVRIEGTYEDSTAVHLVWMLCEGGELFDRIVQKHYSERQARLIKT 120
QY 134 ILGVWACHSLGVMHRDLKPNFLDPSKDDAKLKATDFGLSVFYKPGCYLYDVVVGSPYY 193
Db 121 IVEVWACHSLGVMHRDLKPNFLDFTIDEDAKLKATDFGLSVFYKPGESCDVVVGSPYY 180
QY 194 VAEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETSGIFRQILQKLDKDFKSDPWPPTI 253
Db 181 VAEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETSGIFRQILQKLDKDFHSEPPWPSI 240
QY 254 SEAKDLIVKMLERSPKKISAEALCHPWIVDEQAAPDKPLDPAVLRLKQFQFOMNKK 313
Db 241 SDSAKDLIRKMLDQNPKRLTAHEVLRHPWIVDDNIAPDKPLDSAVLSRLKQFSAWNLK 300
QY 314 KVALRVIARLSSEEEIGGLKELFKMIDTNSGTTTFEELKAGLKVGSSELMESEIKSLMD 373
Db 301 KVALRVIARLSSEEEIGGLKELFKMIDTNSGTTTFEELKAGLKVGSSELMESEIKSLMD 360
QY 374 AADIDNSGTTIDYGEFLAATLHNKMERREILVAAPSDFDKDGSGYITIDELQSACTEFL 433
Db 361 AADIDNSGTTIDYGEFLAATVHLNKLREENTLSAFSYFDKDGSGYITIDELQSACTEFL 420
QY 434 CDTPLDDMIKEIDLNDGKIDFSEFTAMRKGD-GVGRSRTMMK 476
Db 421 DDTHIDDMIKEDQNDGQIDYGEFAAMRKNGGIGR-RTMRK 463

RESULT 7

US-09-347-801-17
; Sequence 17, Application US/09347801
; Patent No. 6262345
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Lee, Jian Ming
; TITLE OF INVENTION: Plant Protein Kinases
; FILE REFERENCE: BB-1171
; CURRENT APPLICATION NUMBER: US/09/347,801
; CURRENT FILING DATE: 1999-07-02
; EARLIER APPLICATION NUMBER: 60/092,438
; EARLIER FILING DATE: July 10, 1998
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Microsoft Office 97

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; SEQ ID NO 17
; LENGTH: 639
; TYPE: PRT
; ORGANISM: Zea mays
US-09-347-801-17

Query Match
Best Local Similarity 64.5%; Score 1672.5; DB 4; Length 639;
Matches 318; Conservative 66; Mismatches 93; Indels 13; Gaps 3;

QY 5 PNRPRPS-----NTVLPYQTPRLRDHYLLGKLGQGGFGTYTLCYCTEKSTASY 52
Db 120 PGRPRPQVQRVSSAGLLGSLVLRKKTENLKDYSGLRGLGQGGFGTTLCLVERATGKEL 179

QY 53 AKSIPKRLVCREDEVDWREIQIWMHLSHNPVRVIRKTYEDSVFVHVMVCSGGEL 112
Db 180 ACSILKRLGSDDDVEDVREIQIMHLAGHPSVVGIRGAYEDAVAVHLVLMELCGGEL 239

QY 113 FDRIVSKGHFSREAVKLITKILGVVEACHSLGVNHRDLKPENFLDPSPKDDAKLKATDF 172
Db 240 FDRIVARGHYTERKAAELARVIVGVVEACHSGMGNVHRDLKPENFLFADHSEEAALKTIDF 299

QY 173 GLSVFYKPGQYLVVVGSPYVAPVLAKEKCPEDVWSAGVILYLLSGVPPFWAETES 232
Db 300 GLSIFPRPGQITDVVGSPYVAPVLAKEKCPEDVWSAGVILYLLSGVPPFWAETES 359

QY 233 GIPRQIOLQKLPKSDPMTTSEAKDLIYKMLERSPKKRISEAHEALCHPMIVDEQAAPD 292
Db 360 GIPEEVLHGRDLDFSESEPSPISDGAADLVRRMLVDRPKRLTAHEVLRHPWQVGGVAPD 419

QY 293 KPLDPAVLSRLKQFSOMNKIKKQALRVIAERLSBEEIGGLKELFKMTDNTSGTITFEEL 352
Db 420 RPLDSAVLSRMKQFSAMNKLKQALRVIAERLSBEEIGGLKELFKMTDNTSGTITFEEL 479

QY 353 KAGLRKVGSELMSEIKSLMDAADINDSGTIDYGEFFAATLHMKNMREILVAATSDFD 412
Db 480 KVGLEKVGANLQESSIYALMQAADVNNGTIDYGEFFAATLHMKNMREILVAATSDFD 539

QY 413 KOGSGYITIDELQASCTEFLGCDTFLDDMIKEIDLNDGKIDFSEFTAMVRKGDGVRGR 472
Db 540 KOGSGYITADELQVACEEFLGCDVLELDLGEVDQDNDGRIDYNEFVAMNQK-PTVGGSR 598

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RESULT 8
US-07-951-715A-22
; Sequence 22, Application US/07951715A
; Patent No. 5625136
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Malini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Leunis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA

```

```

; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA: US/07/951.715A
; FILING DATE: 25-SEP-1992
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Serull, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: S-19805/A/CGC 1577/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8615
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 464 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..464
; OTHER INFORMATION: /note= "derived protein sequence of
; US-07-951-715A-22

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Query Match 55.4%; Score 1437.5; DB 1; Length 464;
Best Local Similarity 60.9%; Pred. No. 6.7e-112;
Matches 271; Conservative 70; Mismatches 103; Indels 1; Gaps 1;

QY 22 LRDEHYLLGKLGQGGFGTYTLCYCTEKSTANVACKSIKRLVCREDEVDWREIQIMHHL 81
Db 9 VRATYSGKELGQGGFGTYTLCYCTEKSTANVACKSIKRLVCREDEVDWREIQIMHHL 69

QY 82 SEHPNVVRKTYEDSVFVHVMVCSGGELFDRIVSKGHFSREAVKLITKILGVVEAC 141
Db 69 SQGPVVVGLRGAYEDKQSVHLMELCAGGELFDRIVSKGHFSREAVKLITKILGVVEAC 128

QY 142 HSLGVNHRDLKPENFLDPSPKDDAKLKATDEGLSVFYKPGQYLVVVGSPYVAPVLAKE 201
Db 129 HSMGVNHRDLKPENFLDPSPKDDAKLKATDEGLSVFYKPGQYLVVVGSPYVAPVLAKE 188

QY 202 CYGPEIDVMSAGVILYLLSGVPPFWAETESGIFRQIOLQKLPKSDPMTTSEAKDLI 261
Db 189 KYGPEADIVMSAGVILYLLSGVPPFWAETESGIFRQIOLQKLPKSDPMTTSEAKDLI 248

QY 262 YKMLERSPKKRISEAHEALCHPMIVDEQAAPDPLDPAVLSRLKQFSOMNKIKKQALRVIA 321
Db 249 KMLNINPRERLTAFOVLAHPMKEDGADPTPLDPAVLSRLKQFSOMNKIKKQALRVIA 308

QY 322 ERLSEEEIGGLKELFKMTDNTSGTITFEELKAGLRKVGSELMSEIKSLMDAADINDSG 381
Db 309 GCLSEEEITGLKEMFNKIDKNSGTTIDELKGLGKLAGHPSVVGIRGAYEDAVAVHLVLMEL 368

QY 382 TIDYGEFFAATLHMKNMREILVAATSDFDKOGSGYITIDELQASCTEFLGCDT-PLDD 440
Db 369 LIIDYGEFFAATLHMKNMREILVAATSDFDKOGSGYITIDELQASCTEFLGCDT-PLDD 428

QY 441 MIKEIDLNDGKIDFSEFTAMVRKGDGVRGR 465
Db 429 IISDADSDNDGRIDYNEFVAMNQK 453

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RESULT 9

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/459.448A
APPLICATION NUMBER: US/08/459.448A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: 40403
REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8582
TELEFAX: (919)541-8699
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 464 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYDROPHETICAL: NO
FEATURE:
NAME/KEY: Protein
LOCATION: 1..464
OTHER INFORMATION: /note= "derived protein sequence of pollen specific CDPK as disclosed in Figure 34."
US-08-459-448A-22

Query Match 55.4%; Score 1437.5; DB 2; Length 464;
Best Local Similarity 60.9%; Pred.No. 6.7e-112;
Matches 271; Conservative 70; Mismatches 103; Indels 1; Gaps: 1;

US-08-459-595A-22
Sequence 22, Application US/08459595A
Patent No. 6018104
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Launis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6018104artis Corporation
STREET: Patent & Trademark Dept., 520 White Plains
ROAD: Rd., POB 2005
CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591-9005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/459.595A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 800

Query Match 55.4%; Score 1437.5; DB 2; Length 464;
Best Local Similarity 60.9%; Pred. No. 6.7e-112;
Matches 271; Conservative 70; Mismatches 103; Indels 1; Gaps 1;
QV 22 LRDHVLLGKLGQGGTGYLTCTEKSTANVACKSIPIKRLKVCNEDYDVWRQIQNHHL 81

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: 40403
REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8582
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 464 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: Protein
LOCATION: 1..464
OTHER INFORMATION: /notes= "derived protein sequence of pollen specific CDPK as disclosed in Figure 34."
US-08-459-595A-22

Query Match 55.4%; Score 1437.5; DB 3; Length 464;
Best Local Similarity 60.9%; Pred. No. 6.7e-112;
Matches 271; Conservative 70; Mismatches 103; Indels 1; Gaps 1;

QY 22 LRHYLLGKLGQGGTGYLTCTEKSTKSTANYACKSIPKRLVCREDYEDVWREIQVHHL 81
DB 9 VRATYSGKELGSGQGVTHLCTHRTSGEKLACKTIARKKLAAREDDVDRREVQVHHL 68
QY 82 SERPNVVRKGTVEDSVFVHVMVECEGELFDRIVSKGHFSEREAVKLKTIILGVVEAC 141
DB 69 SQQPNVVGLRGAYEDKQSVHVMWELCAGELFDRIIARGQYTERGAELLRALVQIVHTC 128
QY 142 HSLGVWHRDLKPNFLDFSKDADKATDFGLSVFYKQVLYDVGVSPYVAPVKK 201
DB 129 HSGVWHRDLKPNFLDFSKDADKATDFGLSVFYKQVLYDVGVSPYVAPVKK 198
QY 202 CYGPEIDWISAGVILYLLSGVPPFWAETESGIFRQILQGLDFKSPWPITSEAAKDLI 261
DB 189 KYGPEADWSGVWLYIFLAGVPPFWAENENGIFTALLRGQLDLSSEPPWHISPGAKDLV 248
QY 262 YKMLSPKPKRISAHALCHPWIVDEQAPDKPLDPAVLRLKQFSQWNIKKWALRVIA 321
DB 249 KKMNLNPKRLTAFOVLAHPWIKEDGADPTPLDNVVDRLKQFRANWQPKAALRRIA 308
QY 322 ERLSEEEIGLKLFRMIDTNSGTTTFEELKAGLRVSGSELMESEIKSLMDADIDNSG 381
DB 309 GCLSEBEITGLKEMFNKIDKNSGTTITLDELKGLAKHGPKLSDSEMKLNEAADGNG 368
QY 382 TIDYGEFLANTLNNKWEREELVIAFSDFDKDGSGYITIDELQSACTEFLCDET-PLDD 440
DB 369 LIDYDEFTVATVHNNKLDREELHYTAFYDFKDSNGYITKEELHAKBQGLYDADKID 428
QY 441 MIKEIDLNDGKIDFSEFTAMRK 465
DB 429 IISDADSNDGRIDYSEFVAMRK 453

RESULT 11
US-08-459-504B-22
Sequence 22, Application US/08459504B
Patent No. 6075185
GENERAL INFORMATION:
APPLICANT: Kozel, Michael G.
APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.

APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Launis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Surtie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6075185artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,504B
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/459,595
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC1577/CIP/DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 464 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: Protein
LOCATION: 1..464
OTHER INFORMATION: /notes= "derived protein sequence of pollen specific CDPK as disclosed in Figure 34."
US-08-459-504B-22

Query Match 55.4%; Score 1437.5; DB 3; Length 464;
Best Local Similarity 60.9%; Pred. No. 6.7e-112;
Matches 271; Conservative 70; Mismatches 103; Indels 1; Gaps 1;

QY 22 LRHYLLGKLGQGGTGYLTCTEKSTKSTANYACKSIPKRLVCREDYEDVWREIQVHHL 81
DB 9 VRATYSGKELGSGQGVTHLCTHRTSGEKLACKTIARKKLAAREDDVDRREVQVHHL 68
QY 82 SERPNVVRKGTVEDSVFVHVMVECEGELFDRIVSKGHFSEREAVKLKTIILGVVEAC 141
DB 69 SQQPNVVGLRGAYEDKQSVHVMWELCAGELFDRIIARGQYTERGAELLRALVQIVHTC 128

142 HSLGVMHDLKPEFLFDSKODAKLKTDFGLSVFYKPGQYLDVVGSPYVAPVLLKK 201
129 HSMGVNHRDIKPEFLLSKDEDAPLKATDFGLSVFYKPGQYLDVVGSPYVAPVLLKK 188
202 CYGPEIDVMSAGVILYLLSGVPPFWAETESGIFRQILOKGLDFKSDPWPPTISEAAKDLI 261
189 KYGPEADVSWGVMLYIFLAGVPPFWAENENGIFTALRGQLDLSSEPPWPHISFGAKDLV 248
262 YKMLERSPKKISAEALCHWIVDEQAAPKPLDPAVLRLKQFOSQNNKIKKMLARVIA 321
249 KMLNINPKERLTAPQVNLNHPWIKEDGAPDTPDNLNVLDRKQFRANQFKKAALRIIA 308
322 ERLSBEIEGGLKELFKMTDNTSGTITPEELKAGLRKRVGSELMESEIKSLMDAADINDSG 381
309 GCLSEIEITGLKEMFNKIDKNSGTITLDELKHLGKXGPKLSDEMEKLMEEAADGNG 368
382 TIDYGEFLAALHNMKREBELVNAFSDPKDGSYITTDLOSACTEGLCDT-PLDD 440
369 LIDYDEFVTATVHNNKLDRHEHLYTAFQYFDKNSGYITKEELEHALKEOGLYDADKIKD 428
441 MIKEIDLNDGKIDSEFTAMMRKG 465
429 IISDADSDNDGRIDYSEFVAMMRKG 453

RESULT 12
US-08-459-444-22
; Sequence 0, Application US/08459444
; Patent No. 6121014
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Lauis, Karen L.
TITLE OF INVENTION: METHOD FOR PRODUCING A PLANT-OPTIMIZED
NUCLEIC ACID CODING SEQUENCE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESS: No. 6121014artis Agribusiness Biotechnology Research, Inc.
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,444A
FILING DATE: 02-Jun-1995
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-18805/P1/CGC1577/CIP/DIV6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: /note= "derived protein sequence of

pollen specific CDPK as disclosed in Figure 34."
SEQUENCE CHARACTERISTICS:
LENGTH: 464 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: Protein
LOCATION: 1..464
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-08-459-444-22
Query Match 55.4%; Score 1437.5; DB 3; Length 464;
Best Local Similarity 60.9%; Pred. No. 6.7e-112;
Matches 271; Conservative 70; Mismatches 103; Indels 1; Gaps 1;
QY 22 LRHYVLLGKLGQSGFTTYLCTEKSTSNANYACKSIPKRLVCREDYEDVWREIQIMHHL 81
Db 9 VRATYSVKELGRQFGVTHLCHTRTSGEKLACKTAKKLAAREDDVDVREVQIMHHL 68
QY 82 SEHPNVVRIKGTYESVFNHVMVEVCGGELFDRIVSKGHFSEREAVKLIKILGVVEAC 141
Db 69 SGQPNVVLGRGAYEDKQSVHLVWELCAGGELFDRITARGQYTERGAELLRAIVQIVHTC 128
QY 142 HSLGVMHDLKPEFLFDSKODAKLKTDFGLSVFYKPGQYLDVVGSPYVAPVLLKK 201
Db 129 HSMGVNHRDIKPEFLLSKDEDAPLKATDFGLSVFYKPGQYLDVVGSPYVAPVLLKK 188
QY 202 CYGPEIDVMSAGVILYLLSGVPPFWAETESGIFRQILOKGLDFKSDPWPPTISEAAKDLI 261
Db 189 KYGPEADVSWGVMLYIFLAGVPPFWAENENGIFTALRGQLDLSSEPPWPHISFGAKDLV 248
QY 262 YKMLERSPKKISAEALCHWIVDEQAAPKPLDPAVLRLKQFOSQNNKIKKMLARVIA 321
Db 249 KMLNINPKERLTAPQVNLNHPWIKEDGAPDTPDNLNVLDRKQFRANQFKKAALRIIA 308
QY 322 ERLSBEIEGGLKELFKMTDNTSGTITPEELKAGLRKRVGSELMESEIKSLMDAADINDSG 381
Db 309 GCLSEIEITGLKEMFNKIDKNSGTITLDELKHLGKXGPKLSDEMEKLMEEAADGNG 368
QY 382 TIDYGEFLAALHNMKREBELVNAFSDPKDGSYITTDLOSACTEGLCDT-PLDD 440
Db 369 LIDYDEFVTATVHNNKLDRHEHLYTAFQYFDKNSGYITKEELEHALKEOGLYDADKIKD 428
QY 441 MIKEIDLNDGKIDSEFTAMMRKG 465
Db 429 IISDADSDNDGRIDYSEFVAMMRKG 453

RESULT 13
US-09-547-422-22
; Sequence 0, Application US/09547422
; Patent No. 6320100
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Lauis, Karen L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESS: No. 6320100artis Agribusiness Biotechnology Research, Inc.
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park

Qy 136 GWEACHSLGVHRLKPENFLFDSPKD
 ; | |||:||||:||||| | :

[illegible]

Db 61 QIVHTCHSGVWHRDIKPENFILLSKDEDAFLKATDFGLSVFFKEGELLRDIVGSAYVIA 120
QY 196 PEVLKCYGPEIDVMSAGVILYLLSGVPPFWAETESGIFQILOGKLDKPSDPNPTISE 255
Db 121 PEVLKRYGPEADIVSGVWMLYIFLAGVPPFWAENENGIFTAILRGQLDLSSEFPWPHISP 180
QY 256 AAKDLIYKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPVLSRLKQFQSONMKIKKM 315
Db 181 GAKDLVKKMLNINPKERLTAQVNLNHPWKEDGDAPDTPLDNVVLDRLKQFRAMNQPKKA 240
QY 316 ALRVIAERLSEIEGGLKELFKQMTDNTSGNITFEELKAGLKRVSGLMSEIEKSLNDAA 375
Db 241 ALRIIAGCLSEIEITGLKEMFNKIDKNSGTTILDELKHLAKHGPKLSSEMEKLMEEA 300
QY 376 DIDNSGTDYGEFLAATLHMKNKVEREILVAAFSDFDKGGSGYITIDELQSACTEFGLCD 435
Db 301 DADGNGLIDYDEFVATVHMKNLDREELHYTAFQYFDKNSGYITKEELHALKEQGLYD 360
QY 436 T-PLDDMIKEIDLNDGKIDFSEFTAMMRKG 465
Db 361 ADKIKDIISDADSDNDGRIDYSEFVAMMRKG 391

RESULT 15

US-08-459-448A-21
Sequence 21, Application US/08459448A
Patent No. 5859336
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Launis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dundez, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5859336artis Corporation
STREET: Patent & Trademark Dept., 520 White Plains
STREET: Rd., POB 2005
CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591-9005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,448A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: 40403

REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8582
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 408 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-448A-21
Query Match 49.3%; Score 1277.5; DB 2; Length 408;
Best Local Similarity 61.9%; Pred. No. 1.2e-98;
Matches 242; Conservative 59; Mismatches 89; Indels 1; Gaps 1;
QY 76 QIMHLSHPNVRKIKTYEDSVFVHIVMEVCEGELFDRIIVSKGHFSEREAVKLIKIL 135
Db 1 QIMHLSGQPNVGLRGAYEDKQSVHLVLMELCAGGELFDRIIARGQYTERGAAELLRAIV 60
QY 136 GVVEACHSLGVNHRDLKPENFLDPSPKDDAKLKATDFGLSVFYKPGQYLYDVVGSPPYVA 195
Db 61 QIVHTCHSGVWHRDIKPENFILLSKDEDAFLKATDFGLSVFFKEGELLRDIVGSAYVIA 120
QY 196 PEVLKCYGPEIDVMSAGVILYLLSGVPPFWAETESGIFQILOGKLDKPSDPNPTISE 255
Db 121 PEVLKRYGPEADIVSGVWMLYIFLAGVPPFWAENENGIFTAILRGQLDLSSEFPWPHISP 180
QY 256 AAKDLIYKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPVLSRLKQFQSONMKIKKM 315
Db 181 GAKDLVKKMLNINPKERLTAQVNLNHPWKEDGDAPDTPLDNVVLDRLKQFRAMNQPKKA 240
QY 316 ALRVIAERLSEIEGGLKELFKQMTDNTSGNITFEELKAGLKRVSGLMSEIEKSLNDAA 375
Db 241 ALRIIAGCLSEIEITGLKEMFNKIDKNSGTTILDELKHLAKHGPKLSSEMEKLMEEA 300
QY 376 DIDNSGTDYGEFLAATLHMKNKVEREILVAAFSDFDKGGSGYITIDELQSACTEFGLCD 435
Db 301 DADGNGLIDYDEFVATVHMKNLDREELHYTAFQYFDKNSGYITKEELHALKEQGLYD 360
QY 436 T-PLDDMIKEIDLNDGKIDFSEFTAMMRKG 465
Db 361 ADKIKDIISDADSDNDGRIDYSEFVAMMRKG 391

Search completed: February 13, 2003, 21:12:42
Job time : 23 secs

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OM protein - protein search, using sw model

Run on: February 13, 2003, 21:11:33 ; Search time 19 Seconds

(without alignments)
665.615 Million cell updates/sec

Title: US-09-848-806-1

Perfect score: 2593

Sequence: 1 METKPNRPSPNTVLPYQTP.....KNLNFNIADAFGVGKSD 495

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 140259 seqs, 25548876 residues

Total number of hits satisfying chosen parameters: 140259

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/prodata/1/pubpaa/US08_NEW_PUB.pcp.*
- 2: /cgn2_6/prodata/1/pubpaa/PCT_NEW_PUB.pcp.*
- 3: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pcp.*
- 4: /cgn2_6/prodata/1/pubpaa/US06_PUBCOMB.pcp.*
- 5: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pcp.*
- 6: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pcp.*
- 7: /cgn2_6/prodata/1/pubpaa/PCTUS_PUBCOMB.pcp.*
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- 10: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pcp.*
- 11: /cgn2_6/prodata/1/pubpaa/US10_NEW_PUB.pcp.*
- 12: /cgn2_6/prodata/1/pubpaa/US10_PUBCOMB.pcp.*
- 13: /cgn2_6/prodata/1/pubpaa/US60_NEW_PUB.pcp.*
- 14: /cgn2_6/prodata/1/pubpaa/US60_PUBCOMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1672.5	64.5	639	10	US-09-854-731-17
2	1509.5	58.2	549	10	US-09-828-313-39
3	849	32.7	597	10	US-09-828-313-38
4	828	32.0	623	10	US-09-854-731-4
5	826	31.9	625	10	US-09-854-731-18
6	800	30.9	576	10	US-09-854-731-19
7	587.5	22.7	317	9	US-09-935-464-36
8	587.5	22.7	370	10	US-09-817-181-4
9	554	21.4	357	9	US-10-024-036B-2
10	543.5	21.0	556	12	US-10-096-960-4
11	543	20.9	460	9	US-09-935-464-3
12	543	20.9	476	9	US-09-935-464-5
13	539	20.8	565	12	US-10-096-960-2
14	538.5	20.8	326	10	US-09-817-181-2
15	533.5	20.6	387	10	US-09-771-161A-188
16	510.5	19.7	648	9	US-10-024-036B-5
17	510.5	19.7	817	10	US-09-992-481-4
18	501	19.3	765	9	US-10-217-357-4
19	501	19.3	765	10	US-09-975-326-4

20	501	19.3	766	9	US-09-934-406-2	Sequence 2, Appli
21	501	19.3	766	9	US-10-217-357-2	Sequence 2, Appli
22	501	19.3	766	10	US-09-975-326-2	Sequence 2, Appli
23	496	19.1	385	9	US-10-116-332-2	Sequence 2, Appli
24	489.5	18.9	454	10	US-09-771-161A-238	Sequence 238, App
25	473	18.2	543	10	US-09-740-627-1	Sequence 1, Appli
26	468.5	18.1	280	10	US-09-835-788A-16	Sequence 16, Appli
27	461.5	17.8	406	10	US-09-771-161A-210	Sequence 210, App
28	460	17.7	261	10	US-09-925-299-983	Sequence 983, App
29	457.5	17.6	740	10	US-09-771-161A-265	Sequence 265, App
30	457.5	17.6	740	10	US-09-771-161A-266	Sequence 266, App
31	453	17.5	522	10	US-09-740-627-11	Sequence 11, Appli
32	447.5	17.3	501	10	US-09-797-039-2	Sequence 2, Appli
33	447.5	17.3	501	12	US-10-153-921-2	Sequence 2, Appli
34	446	17.2	1518	10	US-09-801-368-152	Sequence 152, App
35	445.5	17.2	1203	10	US-09-799-875-5	Sequence 5, Appli
36	443	17.1	514	10	US-09-922-138-5	Sequence 2, Appli
37	443	17.1	514	10	US-09-841-683-2	Sequence 2, Appli
38	437	16.9	465	9	US-10-174-784-2	Sequence 2, Appli
39	435	16.8	661	10	US-09-780-949-2	Sequence 2, Appli
40	435	16.8	661	10	US-09-780-949-6	Sequence 6, Appli
41	433	16.7	388	10	US-09-940-921B-7	Sequence 7, Appli
42	431.5	16.6	424	10	US-09-771-161A-257	Sequence 257, App
43	431.5	16.6	424	10	US-09-771-161A-258	Sequence 258, App
44	431.5	16.6	424	10	US-09-771-161A-259	Sequence 259, App
45	431	16.6	398	10	US-09-940-921B-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1

US-09-854-731-17
; Sequence 17, Application US/09854731
; Patent No. US20020120949A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Lee, Jian Ming
; TITLE OF INVENTION: Plant Protein Kinases
; FILE REFERENCE: BB-1171
; CURRENT APPLICATION NUMBER: US/09/854,731
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/092,438
; PRIOR FILING DATE: July 10, 1998
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 17
; LENGTH: 639
; TYPE: PRT
; ORGANISM: Zea mays
US-09-854-731-17

Query Match 64.5%; Score 1672.5; DB 10; Length 639;
Best Local Similarity 66.2%; Pred No. 1.6e-110;
Matches 318; Conservative 66; Mismatches 83; Indels 13; Gaps 3;

Qy	5	PNPR-RPS-----NTVLPTQPLRLDHYLLGKLGQGGFGTTLCTEKSTSNY	52
Db	120	PSRPRPQVRKVSAGLLGSLVLRKNTENLKDYSIGRLGQGGFGTTLCTEKATGKL	179
Qy	53	ACKSIPKRLVCREDYEDVREIQIMHLSHEPNVVRIGTYEDSVFVHVMVCEGGL	112
Db	180	ACKSILKRLGSDDDVEDVREIQIMHLSHAGPSVVGRCAGADAVAVHLMVLCGGEL	239
Qy	113	FDRTVSGHFSREAVKILNTILGVVVEACHSLGMVHRDLKPNFLFDSFKDAKLATDF	172
Db	240	FDRIVRGHTYTERKAAELARVIGVVVEACHSMGMVHRDLKPNFLFADHSEBAALKTIDF	299
Qy	173	GLSVFYKGGQYLDVVGSPYYVAPVLLKCYGPEIDVWSAGVILYLLSGVPPFVAETES	232
Db	300	GLSIFFRPGQIFTDVVGSPYYVAPVLLKCYGPEIDVWSAGVILYLLSGVPPFVAETES	359
Qy	233	GIFPQIILQGLDKFSPWPPTISEAAKDLIVKMLSPKRRISAHEALCHPWIVDEQAAPD	292

Db 360 GIFEVLHRLDFESEPWPSTSDGAKLVRRMLVRDPKRLTAHEVLRHWPVQGVGAPD 419
 Qy 293 KPLDPAVLSRLKQFSQMNKIKKVALRVIAERLSEEEIGGLKELFPMIDTNSGTTIFEEL 352
 Db 420 RPLDSAVLSRMKQFANVKLKKVALRVIAENLSEDETAGLREMFQMDADNSQITIFEEL 479
 Qy 353 KAGLRKVGSELMESEIKSLMDAADINDSGTIDYGEFFLAATLHMNMREBEILVAAPDFD 412
 Db 480 KVGLEKVGANLQSEIYALMQAADVNNGTIDYGEFFLAATLHNMKVEREHLFAAFQYFD 539
 Qy 413 KDGSYITIDELQSACTEFLGCDTPLDMMIKEIDLNDGKIDRSEFTAMMRKGDGVRGR 472
 Db 540 KDGSYITADELQVACEEFLGCDVLEDLISEVDQDNDGRIDYNEFVAMQK-PTVGSR 598

RESULT 2
 US-09-828-313-39
 ; Sequence 39, Application US/09828313
 ; Patent No. US20020059662A1
 ; GENERAL INFORMATION:
 ; APPLICANT: COSTA e SILVA, OSWALDO DA
 ; APPLICANT: BOHNERT, HANS J.
 ; APPLICANT: THIELEN, NOCHA VAN
 ; APPLICANT: CHEN, ROUYING
 ; APPLICANT: SARRIA-MILLAN, RODRIGO
 ; TITLE OF INVENTION: PROTEIN KINASE STRESS-RELATED PROTEINS AND METHODS OF
 ; FILE REFERENCE: 16313-0032
 ; CURRENT APPLICATION NUMBER: US/09/828,313
 ; PRIOR FILING DATE: 2001-04-06
 ; PRIOR APPLICATION NUMBER: 60/196,001
 ; NUMBER OF SEQ ID NOS: 128
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO 39
 ; LENGTH: 549
 ; TYPE: PRT
 ; ORGANISM: Physcomitrella patens
 US-09-828-313-39

Query Match 58.2%; Score 1509.5; DB 10; Length 549;
 Best Local Similarity 60.8%; Pred. No. 4.1e-99;
 Matches 290; Conservative 70; Mismatches 112; Indels 5; Gaps 3;

Qy 5 PNPRESNT---VLPQTPRLRDHYLLGKLGQGGTGLCTEKSANSVACKSPKPK 61
 Db 69 PRKPASRSVGVLCPLSDIQSILRELGRGQGVLYLCTDKMTNEAYACKSAKK 128
 Qy 62 LVCREYEDVWREIQIMHLSHPNVRIKGTYESVVFHIVMEVCEGGLFDRIVSKGH 121
 Db 129 LTSKEDIEDYKREYQIMHLSGTPNIVVLKDVFDKHSVHLVWMLCAGGLFDRIIAKGH 188
 Qy 122 FSREAVKLIKTLGVVEACHSLGVWHRDLKPNFLDPSPKDDAKLKATDFGLSVFKPG 181
 Db 189 YSREAAACRVIVNVVHRCSLGVFHRDLKPNFLASKAEDAPLKATDFGLSTFKPG 248
 Qy 182 QYLYDVVGSYVYVAPVLKCKYGPIDVMSAGVILYLLSGVPPFWAETSGIFRQLQG 241
 Db 249 DVFQDIYVGSAYYVAPVLKRSYGPEDVMSAGVIVYLLCGVPPFWAETSGIFDAVLKG 308
 Qy 242 KLDKSDPPTISEAAKDLIYKMLERSPKKRISAEALCHPWIIVDEQAAADPKLDPVILS 301
 Db 309 HIOFENDPWFKISNGAKDLVRKMLPNVVKIRLTAQQVNLNHPMKEDGCDPVDLDAVLT 368
 Qy 302 RLKQFSQMNKIKKVALRVIAERLSEEEIGGLKELFPMIDTNSGTTIFEELKAGLRKVG 361
 Db 369 RLKFNFAANKMKKALVKIAESLSSEEEIGLREMPKSIDTNSGTTIFEELKEGLKQGS 428
 Qy 362 ELMESEIKSLMDAADINDSGTIDYGEFFLAATLHMNMREBEILVAAPDFDQKSGYITI 421
 Db 429 KLNESIRKLMEAADVNGKIDPNEFISATWHNNKTEKDEHLWAAFWHFDTNSGYITI 488

Qy 422 DELQSACTEFLGCD-TPLDMMIKEIDLNDGKIDRSEFTAMMRKGD-GVGRSRTMMK 476
 Db 489 DELQSACTEFLGCD-TPLDMMIKEIDLNDGKIDRSEFTAMMRKGD-GVGRSRTMMK 545

RESULT 3
 US-09-828-313-38
 ; Sequence 38, Application US/09828313
 ; Patent No. US20020059662A1
 ; GENERAL INFORMATION:
 ; APPLICANT: COSTA e SILVA, OSWALDO DA
 ; APPLICANT: BOHNERT, HANS J.
 ; APPLICANT: THIELEN, NOCHA VAN
 ; APPLICANT: CHEN, ROUYING
 ; APPLICANT: SARRIA-MILLAN, RODRIGO
 ; TITLE OF INVENTION: PROTEIN KINASE STRESS-RELATED PROTEINS AND METHODS OF
 ; FILE REFERENCE: 16313-0032
 ; CURRENT APPLICATION NUMBER: US/09/828,313
 ; PRIOR FILING DATE: 2001-04-06
 ; PRIOR APPLICATION NUMBER: 60/196,001
 ; NUMBER OF SEQ ID NOS: 128
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO 38
 ; LENGTH: 597
 ; TYPE: PRT
 ; ORGANISM: Physcomitrella patens
 US-09-828-313-38

Query Match 32.7%; Score 849; DB 10; Length 597;
 Best Local Similarity 36.9%; Pred. No. 1.7e-52;
 Matches 203; Conservative 92; Mismatches 163; Indels 92; Gaps 14;

Qy 5 PNPRESNTVLPY-----QTPR----- 21
 Db 62 PSRHPASPLPHYTSTSPAPSTPRRNIFKRPFPSPAKHQQSLVLRHGAKPKGGAIP 121
 Qy 22 -----LRDH-----YLLGKLGQGGTGLCTEKSANSVACKSPKPK 58
 Db 122 EAVDGEKPLDKHFGVHKNFATKYLGEHVEGRGHGHT--CYAKVRKEHGKQAVAVKILS 179
 Qy 59 KRKLVCREDYEDVWREIQIMHLSHPNVRIKGTYESVVFHIVMEVCEGGLFDRIVS 118
 Db 180 KAKMTTAAIEDVGREVKILKALTGHQNLVRFYDSCEDHLNVYIWMELCEGGLDRILS 239
 Qy 119 K-GHFSREAVKLIKTLGVVEACHSLGVWHRDLKPNFLDPSPKDDAKLKATDFGLSVF 177
 Db 240 RGGYSEEDAKVVVRILSVVAFCHLQGVVHRDLKPNFLFTTKDEYTAQLKATDFGLSDP 239
 Qy 178 YKPGQYLYDVVGSYVYVAPVLKCKYGPIDVMSAGVILYLLSGVPPFWAETSGIFRQ 237
 Db 300 IKPDERLNDIVGSAYYVAPVLKRLYLSMEADVMSIGVITYILLGSRPFWARTESGIFRA 359
 Qy 238 ILQGLKDFKSDPKPTISEAAKDLIYKMLERSPKKRISAEALCHPWIIVDEQAAADPKLDP 297
 Db 360 VLRADSFSEAPWPSISPEAKDFVRLNKNMRKMTAAQALTPWIRSNV--KIPLDI 417
 Qy 298 AVLRLKQFSQMNKIKKVALRVIAERLSEEEIGGLKELFPMIDTNSGTTIFEELKAGLR 357
 Db 418 LVYRLVRNVLRASSMRKAALKALSITLDETFVLRTOFMLEPSNNGRVTFFENFQALL 477
 Qy 358 RVGSELM-ESEIKSLMDAADINDSGTIDYGEFFLAATLHMNMREBEILVAAPDFD 412
 Db 478 KNSTEAMKSRVFEILLESMDGLHFKKNDFFSCAAASVLOLEATEREWEQHARAAYDIFE 537
 Qy 413 KDGSYITIDELQSACTEFLGCD-TPLDMMIKEIDLNDGKIDRSEFTAMMRKGDG 468
 Db 538 KEGNRVYIPDEL---AKEMGLAPNVPAQVFLDWIRQ-----SDGRSLFTGTKLH----- 585
 Qy 469 GRSETVMKNL 478
 Db 586 GISSRAIKNL 595

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; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 18
; LENGTH: 625
; TYPE: PRT
; ORGANISM: Zea mays
US-09-854-731-18

Query Match      31.9%; Score 826; DB 10; Length 625;
Best Local Similarity 40.8%; Pred. No. 7.3e-51;
Matches 183; Conservative 85; Mismatches 159; Indels 22; Gaps 10;

QY 26 YLGGKLGQGGFGTTLCTEKS----TSANVACKSIPKRLVCRDVEDVWREIQIMHLS 82
DB 174 YDLGKEVGRGHFGHTCSAVVKKGHEKHGHTVAVKIIISKAKMTAISIEDVREVKILKALS 233
QY 83 EHPNVVRIKGTVEDSVFVHIVMEVCEGELFDRIIVSK-GHFSEREAVKLITLGVVEAC 141
DB 234 GHDNLVRFYDACEALNVIYVMECEGELLDRILARGRYTEEDAKAIIVQLSVVAF 293
QY 142 HSLGVNHRDLKPEFLDPSKDDAKLTKATDFGLSVFVKPGQYLYDVVGVSPYYVAPEVLKK 201
DB 294 HLQGVVHRDLKPEFLFTRDESAPMKLIDFGLSDFIRPDERLNDIVGSAYYVAPEVLHR 353
QY 202 CYGPELDVMSAGVILYLLSGVPPFWAETESGIFRQILQGLDKFSPWPTTISEAAKDLI 261
DB 354 SYSMEADIVSIQVITVYLLCGSRPFWARTESGIFRSVLADPNFDDSPWSPVSAEAKDFV 413
QY 262 YKMLERSPKRISAHEALCHPWIVDEQAAPDKPLDPVLSRLKQFSQMNKIKGMALRVIA 321
DB 414 KRFLNKDYKRWKMTAVQALTHPWLDEQR-QIPLDLIFRLVKQYLRLATPLKRLALKALS 471
QY 322 ERLSEEEIGGLKELFKMIDTNSGITTEELKAGIKRVGSELM-ESEIKSLMDAADIDNS 380
DB 472 KALSEDELLYLRQFKLLE-PRDGFVSLDNFRTALTRYLTDAMKESRVLEFQHALEPLAY 530
QY 381 GTIDYGEFLAATL---HNNKMER-BEILVAAFSPDKDGSYIITIDELQSACTEFGLCDT 436
DB 531 RKNDFEFCAAAISPYQLEALERWEEIAGTAFQFQEQEGNRVISEEL---AQELNLAPT 587
QY 437 P---LDDMIKEIDLNDGKIDFSEPTAMM 462
DB 588 HYSIVQDWIRK----SDGKLNFLGLTKFL 612

RESULT 6
US-09-854-731-19
; Sequence 19, Application US/09854731
; Patent No. US20020120949A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; TITLE OF INVENTION: Plant Protein Kinases
; FILE REFERENCE: BB-1171
; CURRENT APPLICATION NUMBER: US/09/854,731
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/092,438
; PRIOR FILING DATE: July 10, 1998
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 19
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-854-731-19

Query Match      30.9%; Score 800; DB 10; Length 576;
Best Local Similarity 38.1%; Pred. No. 4.5e-49;
Matches 177; Conservative 94; Mismatches 171; Indels 22; Gaps 10;

QY 25 HYLGGKLGQGGFGTTLCTEKSAN-----YACKSIPKRLVCRDVEDVWREIQIMH 79
DB 122 HYEDGVEGRGHFG--YTSACKGKSLKGQEVAVKVIKSKMTTAAIEDVSRVEXMLR 179

; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 18
; LENGTH: 625
; TYPE: PRT
; ORGANISM: Zea mays
US-09-854-731-18

Query Match      31.9%; Score 826; DB 10; Length 625;
Best Local Similarity 40.8%; Pred. No. 7.3e-51;
Matches 183; Conservative 85; Mismatches 159; Indels 22; Gaps 10;

QY 26 YLGGKLGQGGFGTTLCTEKS----TSANVACKSIPKRLVCRDVEDVWREIQIMHLS 82
DB 174 YDLGKEVGRGHFGHTCSAVVKKGHEKHGHTVAVKIIISKAKMTAISIEDVREVKILKALS 233
QY 83 EHPNVVRIKGTVEDSVFVHIVMEVCEGELFDRIIVSK-GHFSEREAVKLITLGVVEAC 141
DB 234 GHDNLVRFYDACEALNVIYVMECEGELLDRILARGRYTEEDAKAIIVQLSVVAF 293
QY 142 HSLGVNHRDLKPEFLDPSKDDAKLTKATDFGLSVFVKPGQYLYDVVGVSPYYVAPEVLKK 201
DB 294 HLQGVVHRDLKPEFLFTRDESAPMKLIDFGLSDFIRPDERLNDIVGSAYYVAPEVLHR 353
QY 202 CYGPELDVMSAGVILYLLSGVPPFWAETESGIFRQILQGLDKFSPWPTTISEAAKDLI 261
DB 354 SYSMEADIVSIQVITVYLLCGSRPFWARTESGIFRSVLADPNFDDSPWSPVSAEAKDFV 413
QY 262 YKMLERSPKRISAHEALCHPWIVDEQAAPDKPLDPVLSRLKQFSQMNKIKGMALRVIA 321
DB 414 KRFLNKDYKRWKMTAVQALTHPWLDEQR-QIPLDLIFRLVKQYLRLATPLKRLALKALS 471
QY 322 ERLSEEEIGGLKELFKMIDTNSGITTEELKAGIKRVGSELM-ESEIKSLMDAADIDNS 380
DB 472 KALSEDELLYLRQFKLLE-PRDGFVSLDNFRTALTRYLTDAMKESRVLEFQHALEPLAY 530
QY 381 GTIDYGEFLAATL---HNNKMER-BEILVAAFSPDKDGSYIITIDELQSACTEFGLCDT 436
DB 531 RKNDFEFCAAAISPYQLEALERWEEIAGTAFQFQEQEGNRVISEEL---AQELNLAPT 587
QY 437 P---LDDMIKEIDLNDGKIDFSEPTAMM 462
DB 588 HYSIVQDWIRK----SDGKLNFLGLTKFL 612

RESULT 6
US-09-854-731-19
; Sequence 19, Application US/09854731
; Patent No. US20020120949A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; TITLE OF INVENTION: Plant Protein Kinases
; FILE REFERENCE: BB-1171
; CURRENT APPLICATION NUMBER: US/09/854,731
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/092,438
; PRIOR FILING DATE: July 10, 1998
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 19
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-854-731-19

Query Match      30.9%; Score 800; DB 10; Length 576;
Best Local Similarity 38.1%; Pred. No. 4.5e-49;
Matches 177; Conservative 94; Mismatches 171; Indels 22; Gaps 10;

QY 25 HYLGGKLGQGGFGTTLCTEKSAN-----YACKSIPKRLVCRDVEDVWREIQIMH 79
DB 122 HYEDGVEGRGHFG--YTSACKGKSLKGQEVAVKVIKSKMTTAAIEDVSRVEXMLR 179
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QY 80 HLEHNPVRIKGTYESVFIHVMVECEGELFDRIYVK-GHSEAEVXLIKTILGV 138
DB 180 ALTGKRLVQVDAFEDDENNVYVMECKGSGELDKILQGGKYESDDAKVMQVILSV 239
QY 139 EACSHGVNHRDLKPNFLFDSGPKDDAKLKATDFGLSVFYKQGLYLDVWGSPPYVAPEV 198
DB 240 AYCHLQGVHRLDKPNFLFSTKDETSPLKALDFGLSDVVKPDERLNDVGSAYYVAPEV 299
QY 199 LKCYGPEIDVWAGVILYLLSGVPPFWAETESGIFRQILQGLDKDEKSDPWTISEAAK 258
DB 300 LHRTYGTADWMSIGVIAYILLGSGRPFVARTESGIFRAVLKAEFNEEAWPSPPEAV 359
QY 259 DLVXMLERSPKKRIKAHEALCHPWIVDEQAAPDKPLDPAVLRLKQFSQMNKIKK 314
DB 360 DFVKRLNKKYRKLTAQAALCHPLVGSHEL-KIPSDMIYKLVKVMYIMSTSLKRSALA 418
QY 319 VIARLESEBIGGKELFKMIDTDSNGTTFBELKAGLKVGSSELM-ESEIKSLMDAADI 377
DB 419 ALAKTLVPOLAVLREQFTLLGFSKNGYISMQNYKTAILKSTDKMKDSRVDFVHMISC 478
QY 378 DNSGTIDYGEFLAATLHMKNVER---EELVAAFSDFDKSGSYITIDELQSACTEFL 433
DB 479 LOYKGLDFEFECASALSVYOLEAMETWEQHARRAYELFEKGNRPIMIEELAS---ELGL 535
QY 434 -CDTPLDDMTKIBLDNDGKIDSEFTAMMRKGGVGRSRMTWK 476
DB 536 GPSVPEVHVVLQDWIRHSDGKLSFLGFRLLH---GVS-SRTLOK 575
RESULT 7
US-09-935-464-36
; Sequence 36, Application US/09935464
; Publication No. US20030027153A1
; GENERAL INFORMATION:
; APPLICANT: Meyer, Joanne
; APPLICANT: Barrington-Martin, Rory
; APPLICANT: Parker, Alexander
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING NEUROPSYCHIA
; FILE REFERENCE: 3322/1H702 US1
; CURRENT APPLICATION NUMBER: US/09/935,464
; PRIOR FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: US 09/757,300
; PRIOR FILING DATE: 2001-01-09
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: Patent version 3.0
; SEQ ID NO 36
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-464-36
Query Match 22.7%; Score 597.5; DB 9; Length 317;
Best Local Similarity 41.6%; Pred. No. 2.1e-34;
Matches 124; Conservative 55; Mismatches 114; Indels 5; Gaps 4;
GENERAL INFORMATION:
APPLICANT: Bandaru, Rajasekhar
TITLE OF INVENTION: 68730 and 69112, Protein Kinase
TITLE OF INVENTION: Molecules and Uses Therefor
FILE REFERENCE: MEI2000-521P1R(M)
CURRENT APPLICATION NUMBER: US/10/024,036B
PRIOR FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: 60/258222
PRIOR FILING DATE: 2000-12-22
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 357
TYPE: PRT
ORGANISM: Homo sapiens
US-10-024-036B-2

QY 257 AKDLIYKMLERSPKKRIKAHEALCHPWIVDEQAAPDKPLDPAVLRLKQFSQMNKIKK 314
DB 239 AKDFIRHLMKDEPKRFTCEQALQHPWIAGDTAL-DKNTHQSVSEQIKKNFAKSKWKQ 295
RESULT 8
US-09-817-181-4
; Sequence 4, Application US/09817181
; Patent No. US20020142427A1
; GENERAL INFORMATION:
; APPLICANT: MERKULOV, Gennady et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CLO01189
; CURRENT APPLICATION NUMBER: US/09/817,181
; CURRENT FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Human
US-09-817-181-4
Query Match 22.7%; Score 587.5; DB 10; Length 370;
Best Local Similarity 41.6%; Pred. No. 2.5e-34;
Matches 124; Conservative 55; Mismatches 114; Indels 5; Gaps 4;
GENERAL INFORMATION:
APPLICANT: Bandaru, Rajasekhar
TITLE OF INVENTION: 68730 and 69112, Protein Kinase
TITLE OF INVENTION: Molecules and Uses Therefor
FILE REFERENCE: MEI2000-521P1R(M)
CURRENT APPLICATION NUMBER: US/10/024,036B
PRIOR FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: 60/258222
PRIOR FILING DATE: 2000-12-22
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 357
TYPE: PRT
ORGANISM: Homo sapiens
US-10-024-036B-2
Query Match 21.4%; Score 554; DB 9; Length 357;
Best Local Similarity 37.1%; Pred. No. 5.5e-32;
GENERAL INFORMATION:
APPLICANT: Bandaru, Rajasekhar
TITLE OF INVENTION: 68730 and 69112, Protein Kinase
TITLE OF INVENTION: Molecules and Uses Therefor
FILE REFERENCE: MEI2000-521P1R(M)
CURRENT APPLICATION NUMBER: US/10/024,036B
PRIOR FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: 60/258222
PRIOR FILING DATE: 2000-12-22
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 357
TYPE: PRT
ORGANISM: Homo sapiens
US-10-024-036B-2

Matches 117; Conservative 66; Mismatches 120; Indels 12; Gaps 6;

QY 32 LQGGGFTTCTCKSTKSTANYACKSIPKRLKVCSEYEDVWREIQNHLSHPNVRIK 91
 Db 29 LQGAPEVLAEEKATGKLFACIKPKALGKE--SSINEIAVURKI-KHENIVALE 85

QY 92 GTYDSVFVHIMEVCEGELFDRIVSKGHFSEAEVKLTKTLGVVEACHSLGVMRDL 151
 Db 86 DIYESPNHLYLMQVSGELFDRIVEKGFYTEKDASTLIRQLVDVAVYLRMGIVRDL 145

QY 152 KPENFLPSPKDDAKLKATDGLSVFYKPGQYLVDVVGSPYVAPVL-KKCYGPELDVW 210
 Db 146 KPENLXYQSDEESKIMSDPGLSKQEGKGVMTAGCTPGYVAPELAOKPYSKAVDCW 205

QY 211 SAGVILYILLGVPFPFAETSGIFRQILQGLDFKDPNPTISEAAKDIYKMLERSPK 270
 Db 206 SIGVAYILLGVPFPFENDSKLFEQILKAEYBFDSPYMDISDSAKDFIRNLMEKDPN 265

QY 271 KRISAEALCHPWIVDQAAKPKDPAVLSRL-KQPSQMNKIKKMLRVIARELSEEEI 329
 Db 266 KYTCEQAARHPWIAQDTAL-NKNIHESVSAQIRKNFAKSKWQAFNATAVVRHMRKLHL 324

QY 330 GGLKELFKMIDTDS 344
 Db 325 G-----SSLDSNA 333

RESULT 10
 US-10-096-960-4
 ; Sequence 4, Application US/10096960
 ; Publication No. US20020132325A1
 ; GENERAL INFORMATION:
 ; APPLICANT: YE, Jane et al.
 ; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
 ; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
 ; FILE OF INVENTION: THEREOF
 ; FILE REFERENCE: CL001158D1V
 ; CURRENT APPLICATION NUMBER: US/10/096,960
 ; CURRENT FILING DATE: 2002-03-14
 ; PRIOR APPLICATION NUMBER: 09/800,960
 ; PRIOR FILING DATE: 2001-03-08
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 556
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 ; US-10-096-960-4

Query Match 21.0%; Score 543.5; DB 12; Length 556;
 Best Local Similarity 37.0%; Pred. No. 5.2e-31;
 Matches 120; Conservative 63; Mismatches 128; Indels 13; Gaps 5;

QY 21 RLBDHYLLKGLKGGGFTTCTCKSTKSTANYACKSIPKRLKVCSEYEDVWREIQNH 80
 Db 9 RFTDDYQLFEELGKGAFSVVRCKVTSTQEYAAKIINTKLSAR-DHOKLEREARIC-R 66

QY 81 LSEHPNVVRIRKTYEDSVFVHIMEVCEGELFDRIVSKGHFSEAEVKLTKTLGVVEA 140
 Db 67 LLKHPNIVRLHDSISEGTHYLVFDLVTGGELEFEDIVAREYSEADASHCIHQILES 126

QY 141 CHSLGVNHRDLKPENFLPSPKDDAKLKATDGLSVFYKPGQYL-YDVVGSPYVAPVL 199
 Db 127 IHQHDIVHRDLKPENFLPSPKDDAKLKATDGLSVFYKPGQYL-YDVVGSPYVAPVL 186

QY 200 KK-CYGEIDVMSAGVILYLLSGVPPFWAETESGIFRQILQGLDFKSDPWTISEAK 258
 Db 187 RKDPYKPDVIMACGVILYLLSGVPPFWAETESGIFRQILQGLDFKSDPWTISEAK 246

QY 259 DLTYKMLERSPKKRISAEALCHPWIVDEQAAPDKPLDPAVLSRLKQPSQMNKIKMALR 318
 Db 247 NLINQMLTINPAKRITADQALKHPWVQCORSTVASMHRQETVECLRKFNARRKLKALT 306

QY 319 VI-----AERLSEEEIGGLK 333
 Db 307 TMLVSRNFSAAKSLLNKKSGGVK 330

RESULT 11
 US-09-935-464-3
 ; Sequence 3, Application US/09935464
 ; Publication No. US20030027153A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Meyer, Joanne
 ; APPLICANT: Barrington-Martin, Rory
 ; APPLICANT: Parker, Alexander
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING NEUROPSYCHIA
 ; TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA
 ; FILE REFERENCE: 3322/1H702 US1
 ; CURRENT APPLICATION NUMBER: US/09/935,464
 ; CURRENT FILING DATE: 2001-08-23
 ; PRIOR APPLICATION NUMBER: US 09/757,300
 ; PRIOR FILING DATE: 2001-01-09
 ; NUMBER OF SEQ ID NOS: 90
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 3
 ; LENGTH: 460
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-935-464-3

Query Match 20.9%; Score 543; DB 9; Length 460;
 Best Local Similarity 39.6%; Pred. No. 4.5e-31;
 Matches 116; Conservative 62; Mismatches 107; Indels 8; Gaps 6;

QY 18 QTPRLRDHYLLKGLKGGGFTTCTCKSTKSTANYACKSIPKRLKVCSEYEDVWREIQI 77
 Db 15 QTTIRKRTFFMEVVGSGAETSEVPLVKQRITKGLFALKCIKSPAFRDSLEN--EIAV 71

QY 78 MHLSEHPNVVRIRKTYEDSVFVHIMEVCEGELFDRIVSKGHFSEAEVKLTKTLGV 137
 Db 72 LKKI-KHENIVTLEDIYESTTHYVLNQLVSGGELFDRILRGVYTEKDALVIOQVLSA 130

QY 138 VEACHSLGVNHRDLKPENFLPSPKDDAKLKATDGLSVFYKPGQYLVDVVGSPYVAP 197
 Db 131 VKYLHENGIVHRDLKPENFLPSPKDDAKLKATDGLSVFYKPGQYLVDVVGSPYVAP 189

QY 198 VL-KKCYGPEIDVMSAGVILYLLSGVPPFWAETESGIFRQILQGLDFKSDPWTISEA 256
 Db 190 VLAQPYSKAVDCHWSIGVITVYLLCGYPPEETESKLFKIKEGYVEFSPFWDISES 249

QY 257 AKDLIYKMLERSPKKRISAEALCHPWIVDEQAAPDKPLDPAV-LSRLKQPSQ 308
 Db 250 AKDFTCHLEKDPNERYTCEKALSHPMI-DGNTALHRDIYPSVLSIQKNFAK 301

RESULT 12
 US-09-935-464-5
 ; Sequence 5, Application US/09935464
 ; Publication No. US20030027153A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Meyer, Joanne
 ; APPLICANT: Barrington-Martin, Rory
 ; APPLICANT: Parker, Alexander
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING NEUROPSYCHIA
 ; TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA
 ; FILE REFERENCE: 3322/1H702 US1
 ; CURRENT APPLICATION NUMBER: US/09/935,464
 ; CURRENT FILING DATE: 2001-08-23
 ; PRIOR APPLICATION NUMBER: US 09/757,300
 ; PRIOR FILING DATE: 2001-01-09
 ; NUMBER OF SEQ ID NOS: 90
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 5
 ; LENGTH: 476
 ; TYPE: PRT

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; ORGANISM: Homo sapiens
US-09-935-464-5

Query Match      20.9%; Score 543; DB 9; Length 476;
Best Local Similarity 39.6%; Pred. No. 4.7e-31;
Matches 116; Conservative 62; Mismatches 107; Indels 8; Gaps 6;

QY 18 QPRLRDHYLLGKLGQGGFTTYLCTEKSTSANVACKSIKPKLVLCREDYEDVWREIQI 77
DB 15 QTNINRKTIFNEVLGSGAFSEVFLVKGELTCKLPALCKIKKSAFRDSSLEN--EIAV 71

QY 78 MHLSEHPNVRIKGYEDSVFVHIVMEVCEGELFDRIIVSKGHFSEAEVKLTKILGV 137
DB 72 LKKI-KHENIVLTIEDIYESTHYLVLMQVSGGELFDRIILRGVYTERKASLVQQVLSA 130

QY 138 VEACHSLGVMHDLKPENFLFSPKDDAKLKATDFGLSVFKPGQYLDVVGSPYYVAPE 197
DB 131 VKYLHENGIVHRDLKPENLVLTPENSKIMLTFGLSKMEQNG-IMSTAGTGYVAPE 189

QY 198 VL-KCYGPEIDVMSAGVILYILLSGVPPFMAETESGIFRQLQKLDKSDPWTPTISEA 256
DB 190 VLAQKPYKAVDCWSIGVITYILLCGYPPEYETESKLPKIKEGYEFESFPFWDIDISES 249

QY 257 AKOLIYKMLERSPKKRIISAHEALCHPWIVDEQAAPDKPDPAPV-LSRLKQFSQ 308
DB 250 AKOFICHLLEKOPNERYTCEKALSHPWI-DGNALHRDIYPSVLSIQIQNPAK 301

RESULT 13
US-10-096-960-2
; Sequence 2; Application US/10056960
; Patent No. US20020132325A1
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001158DIV
; CURRENT APPLICATION NUMBER: US/10/096,960
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 09/800,960
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 565
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-096-960-2

Query Match      20.8%; Score 539; DB 12; Length 565;
Best Local Similarity 39.0%; Pred. No. 1.1e-30;
Matches 115; Conservative 58; Mismatches 118; Indels 4; Gaps 4;

QY 21 RLRDHYLLGKLGQGGFTTYLCTEKSTSANVACKSIKPKLVLCREDYEDVWREIQIMHH 80
DB 9 RPTDDYQLFEELGKGAFSVVRCKVKTSTOEYAAKIINTKLSAR-DHQKLESEARIC-R 66

QY 81 LSEHPNVRIKGYEDSVFVHIVMEVCEGELFDRIIVSKGHFSEAEVKLTKILGWAEA 140
DB 67 LKHNIVLHDSISEEGFHYLVFLDVTGELFEDIAREYSEADASHCIHQILSSVNH 126

QY 141 CHSLGVMHDLKPENFLFSPKDDAKLKATDFGLSVFKPGQYLDVVGSPYYVAPEVL 199
DB 127 IHQHDIVHRDLKPENLVLTPENSKIMLTFGLSKMEQNG-IMSTAGTGYVAPE 186

QY 200 KK-CYGPEDVMSAGVILYILLSGVPPFMAETESGIFRQLQKLDKSDPWTPTISEAAK 258
DB 187 RKDPTGKPDVIMAGVILYILLGVPPFDEQHKLVQIKAGAYDPPSPENDVTVPPEAK 246

QY 259 DLIYKMLERSPKKRIISAHEALCHPWIVDEQAAPDKPDPAPVLSRLKQFSQNMKIK 313
DB 247 NLINQMLTINPAKRITADQALKHPWVCQRSTVASMHRQETVECLRFENARRKLK 301

; ORGANISM: Homo sapiens
US-09-817-181-2
; Sequence 2; Application US/09817181
; Patent No. US20020142427A1
; GENERAL INFORMATION:
; APPLICANT: MERKULOV, Gennady et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001189
; CURRENT APPLICATION NUMBER: US/09/817,181
; CURRENT FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 326
; TYPE: PRT
; ORGANISM: Human
US-09-817-181-2

Query Match      20.8%; Score 538.5; DB 10; Length 326;
Best Local Similarity 42.8%; Pred. No. 6.1e-31;
Matches 107; Conservative 53; Mismatches 87; Indels 3; Gaps 3;

QY 66 EDEYDVWREIQIMHLSHPNVRIKGYEDSVFVHIVMEVCEGELFDRIIVSKGHFSE 125
DB 14 EDIRDIYDPRDLGTI-KHPNIVALDDIYESGCHLYLIMQLVSGGELFDRIIVEKGFYTER 72

QY 126 EAVKLKILTVGVEACHSLGVMHDLKPENFLFSPKDDAKLKATDFGLSVFKPGQYLY 185
DB 73 DASRLIFQVLDVAVKYLHDLGIVHRDLKPENLVLTPENSKIMLTFGLSKMEQNG 132

QY 186 DVVGSPYYVAPEVL-KCYGPEIDVMSAGVILYILLSGVPPFMAETESGIFRQLQKLD 244
DB 133 TAGCTGYVAPEVLAQKPYKAVDCWSIGVITYILLCGYPPEYDENDAKLEFEQILKAEYE 192

QY 245 FKSDPWTPTISEAAKOLIYKMLERSPKKRIISAHEALCHPWIVDEQAAPDKPDPAPVLSRLK 304
DB 193 FDSYPWDDISDAKDFIRHLMKDEKFTCEQALQHPWIAGDTAL-DKNIHQSVSEQIK 251

QY 305 QFSQNMKIKK 314
DB 252 KNFAKSKWKQ 261

RESULT 15
US-09-771-161A-188
; Sequence 188; Application US/09771161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 188
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-188

Query Match      20.6%; Score 533.5; DB 10; Length 387;
Best Local Similarity 37.0%; Pred. No. 1.7e-30;
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Search completed: February 13, 2003, 21:18:42
Job time : 20 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 13, 2003, 21:04:42 ; Search time 38 Seconds

(without alignments)
1252.277 Million cell updates/sec

Title: US-09-848-806-1

Perfect score: 2593

Sequence: 1 METKPNRPSTNVLPTQTP.....KNLNFNIADAFGVDEKSD 495

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 73:*

1: piri:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2593	100.0	495	1 S46284	calcium-dependent
2	2458	94.8	501	2 G85097	hypothetical prote
3	2030	78.3	490	2 T08873	calcium-dependent
4	1944	75.0	508	1 A43713	calcium-dependent
5	1847.5	71.2	490	1 S71776	calcium-dependent
6	1752	67.6	492	1 T03271	calcium-dependent
7	1751	67.5	487	1 S71770	calcium-dependent
8	1745	67.3	554	1 T03263	calcium-dependent
9	1742	67.2	556	2 T06126	calcium-dependent
10	1731	66.8	544	2 D84550	probable calmoduli
11	1724	66.5	610	1 A49082	calcium-dependent
12	1709.5	65.9	573	2 T09940	calcium-dependent
13	1700.5	65.6	484	2 T05650	calcium-dependent
14	1672.5	64.5	639	1 T02784	calcium-dependent
15	1640.5	63.3	593	2 H84810	probable calcium-d
16	1630	62.9	451	2 S56717	calcium-dependent
17	1586	61.2	542	1 S56651	calcium-dependent
18	1484.5	57.3	540	1 T01989	calcium-dependent
19	1482	57.2	531	2 D85059	probable calcium d
20	1482	57.2	533	1 S56652	calcium-dependent
21	1480	57.1	531	1 T02993	calcium-dependent
22	1453.5	56.4	521	2 G96543	calcium-dependent
23	1462	56.4	529	1 S71774	calcium-dependent
24	1460.5	56.3	513	1 T02259	calcium-dependent
25	1460	56.3	534	1 JC1515	calcium-dependent
26	1458.5	56.2	538	2 T08874	calcium-dependent
27	1449	55.9	554	2 T05476	calcium-dependent
28	1437.5	55.4	465	1 T03024	calcium-dependent
29	1432.5	55.2	532	2 T14335	protein kinase, ca

30	1431	55.2	514	2 T10938	calcium-dependent
31	1381	53.3	545	2 H86322	calcium-dependent
32	1367.5	52.7	493	1 S46283	calcium-dependent
33	1363	52.6	541	2 F96776	hypothetical prote
34	1361	52.5	553	1 T02139	calcium-dependent
35	1356.5	52.3	520	2 F85059	probable calcium d
36	1325.5	51.1	560	2 T46189	calcium-dependent
37	1324.5	51.1	425	2 S17759	protein kinase, ca
38	1313.5	50.7	533	1 S71778	calcium-dependent
39	1287.5	49.7	520	2 A84774	probable calcium-d
40	1280.5	49.4	530	2 A84847	probable Ca2+ depe
41	1238.5	47.8	582	2 E84721	probable calcium-d
42	1229.5	47.4	575	2 C85059	calcium-dependent
43	1225.5	47.3	503	2 T51156	calcium-stimulated
44	1176.5	45.4	591	2 S54788	calcium-dependent
45	1056.5	40.7	571	2 T00835	calcium-dependent

ALIGNMENTS

RESULT 1

S46284
calcium-dependent protein kinase (EC 2.7.1.1-) 2 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 16-Jun-2000
C:Accession: S46284
R:Urao, T.; Katagiri, T.; Mizoguchi, T.; Yamaguchi-Shinozaki, K.; Hayashida, N.; Shinozaki, M. Gen. Genet. 244, 331-340, 1994
A:Title: Two genes that encode Ca(2+)-dependent protein kinases are induced by drought
A:Reference number: S46283; MUID:94359455; PMID:8078458
A:Accession: S46284
A:Molecule type: mRNA
A:Residues: 1-495 <URA>
A:Cross-references: EMBL:D21806; NID:G1235717; PIDN:BA04830.1; PID:G604881
C:Genetics:
A:Gene: CDPK2
C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein ki
C:Keywords: ATP; calcium binding; EF hand; phosphotransferase; serine/threonine-specifi
F:24-284/Domain: protein kinase homology <KIN>
F:32-40/Region: protein kinase ATP-binding motif
F:327-359/Domain: calmodulin repeat homology <EF1>
F:363-395/Domain: calmodulin repeat homology <EF2>
F:399-431/Domain: calmodulin repeat homology <EF3>
F:433-465/Domain: calmodulin repeat homology <EF4>
F:55/Active site: Lys #status predicted

Query Match 100.0%; Score 2593; DB 1; Length 495;
Best Local Similarity 100.0%; Pred. No. 1.6e-99;
Matches 495; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	METKPNRPSTNVLPTQTPRLRDHYLLGKLGQGFQGTTLCTEKSTSANVACKSIPIKR	60
Db	1	METKPNRPSTNVLPTQTPRLRDHYLLGKLGQGFQGTTLCTEKSTSANVACKSIPIKR	60
Qy	61	KLVCREDYEDVWREIQIMHLSHPNVRKITYEDSVFVHIVMEVCEGGLFDRIVSKG	120
Db	61	KLVCREDYEDVWREIQIMHLSHPNVRKITYEDSVFVHIVMEVCEGGLFDRIVSKG	120
Qy	121	HFSEREAVKLIKTLGVWBSACHSLGVMHRDLKPNFLDPSPKDDAKLKATDFGLSVFYKP	180
Db	121	HFSEREAVKLIKTLGVWBSACHSLGVMHRDLKPNFLDPSPKDDAKLKATDFGLSVFYKP	180
Qy	181	GQVLYDVVGSPYYVAPEVLKCKYGPIDVMSAGVILYLLSGVPPFWAETSGIFRQILQ	240
Db	181	GQVLYDVVGSPYYVAPEVLKCKYGPIDVMSAGVILYLLSGVPPFWAETSGIFRQILQ	240
Qy	241	GKLDPKSDPPTTISEAAKOLIKMLERSPKKRIISAHEALCHPWIDEQAAPKPLDPAVL	300
Db	241	GKLDPKSDPPTTISEAAKOLIKMLERSPKKRIISAHEALCHPWIDEQAAPKPLDPAVL	300
Qy	301	SRLKQFSQMNKIKMALRVAERLSEEEIGGLKELFMIDTNSGTTITFEELKAGLRKV	360

Db 301 SRLKQFSQMNKIKKVALRVIAERLSEEEIGGLKELFKMIDTNSGTTITFEELKAGLKEVG 360
Qy 361 SELMESIKSLMDAADIDNSGTTIDYGEFLAATLHNKMEREEILVAAESDPKQSGYIT 420
Db 361 SELMESIKSLMDAADIDNSGTTIDYGEFLAATLHNKMEREEILVAAESDPKQSGYIT 420
Qy 421 IDELQSACTEFLGLCDPLDDMIKEIDLNDGKIDFSEFTAMMRKGDGVRSRRTMMKNLNF 480
Db 421 IDELQSACTEFLGLCDPLDDMIKEIDLNDGKIDFSEFTAMMRKGDGVRSRRTMMKNLNF 480
Qy 481 NIADAFGVDGKSD 495
Db 481 NIADAFGVDGKSD 495
RESULT 2
C85097
hypothetical protein AT4g09570 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 23-Mar-2001
C:Accession: G85097
R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
Nature 402, 769-777, 1999
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: A85001; MUID:20083488; PMID:10611798
A:Accession: G85097
A:Status: preliminary
A:Map position: 4
A:Molecule type: DNA
A:Residues: 1-501 <STO>
C:Cross-references: GB:NC_001268; NID:g2767652; PIDN:CAB78080.1; GSPDB:GN00140
C:Genetics:
A:Gene: AT4g09570
A:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein ki
C:Keywords: EF hand
Query Match 94.8%; Score 2458; DB 2; Length 501;
Best Local Similarity 94.8%; Pred. No. 1.6e-84;
Matches 470; Conservative 9; Mismatches 13; Indels 4; Gaps 1;
Qy 4 KPNRRPNTVLPLYOTPLRDHYLLGKLGQGGTGYLTCTEKSTSNANYACKSIKPKKL 63
Db 3 KPNRRPNSVLPYETPLRDHYLLGKLGQGGTGYLTCTEKSSSNANYACKSIKPKKL 62
Qy 64 CREDYEDVREIQIMHLSHPNVRIKGTVEDSVFVHIVMEVCEGGELFDRIVSKGHFS 123
Db 63 CREDYEDVREIQIMHLSHPNVRIKGTVEDSVFVHIVMEVCEGGELFDRIVSKGCF 122
Qy 124 EREAVKLITLGVVEACHSLGVMHRDLKPNFLFDSPKODAKLKATDFGLSVFPKQY 183
Db 123 EREAAKLITLGVVEACHSLGVMHRDLKPNFLFDSPDDAKLKATDFGLSVFPKQY 182
Qy 184 LYDVVGSPPYVAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFRQILQGL 243
Db 183 LYDVVGSPPYVAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFRQILQGI 242
Qy 244 DFKSDPWPITSEAAKDLIYKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAVL 303
Db 243 DFKSDPWPITSEAKDLIYKMLDRSPKKRISAHEALCHPWIVDESHAAPDKPLDPAVL 302
Qy 304 QFSQMNKIKKVALRVIAERLSEEEIGGLKELFKMIDTNSGTTITFEELKAGLKEVGSEL 363
Db 303 QFSQMNKIKKVALRVIAERLSEEEIGGLKELFKMIDTNSGTTITFEELKAGLKEVGSEL 362
Qy 364 MESEIKSLMDAADIDNSGTTIDYGEFLAATLHNKMEREEILVAAESDPKQSGYITIDE 423
Db 363 MESEIKSLMDAADIDNSGTTIDYGEFLAATLHNKMEREEILVAAESDPKQSGYITIDE 422
Qy 424 LQSACTEFLGLCDPLDDMIKEIDLNDGKIDFSEFTAMMRKGDGVRSRRTMMKNLNF 483
Db 423 LQSACTEFLGLCDPLDDMIKEIDLNDGKIDFSEFTAMMRKGDGVRSRRTMMKNLNF 482
Qy 484 DAFGVDG----EKSD 495

Db 483 EAFGVEDTSTAKSD 498
RESULT 3
T08873
calcium-dependent protein kinase (EC 2.7.1.1-) beta - soybean
C:Species: Glycine max (soybean)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jan-2000
C:Accession: T08873
R:Lee, J.Y.; Yoo, B.C.; Harmon, A.C.
submitted to the EMBL Data Library, September 1996
A:Reference number: Z16505
A:Accession: T08873
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-490 <LEE>
A:Cross-references: EMBL:U69173; NID:g2501763; PID:g2501764
C:Genetics:
A:Gene: CDPK beta
C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein ki
C:Keywords: ATP; calcium binding; EF hand; phosphotransferase; serine/threonine-specifi
F:22-282/Domain: protein kinase homology <kin>
F:30-38/Region: protein kinase ATP-binding motif
F:324-356/Domain: calmodulin repeat homology <EPH>
F:53/Active site: Lys #status Predicted
Query Match 78.3%; Score 2030; DB 2; Length 490;
Best Local Similarity 81.1%; Pred. No. 1e-68;
Matches 386; Conservative 43; Mismatches 45; Indels 2; Gaps 2;
Qy 14 VLPYQTPRLRDHYLLGKLGQGGTGYLTCTEKSTSNANYACKSIKPKKLVCREDYEDV 73
Db 12 VLPYQTPARLDHYLVGLKLGQGGTGYLTCTHKVTGKLYACKSIKPKKLVCREDYEDV 71
Qy 74 EIQIMHLSHPNVRIKGTVEDSVFVHIVMEVCEGGELFDRIVSKGHFSREAVKL 133
Db 72 EIQIMHLSHPNVQIQGYEDSVFVHIVMEVCEGGELFDRIIQKGYHSEAAKL 131
Qy 134 ILGVVEACHSLGVMHRDLKPNFLFDSPKODAKLKATDFGLSVFPKQYLYDVVGSPPY 193
Db 132 IVGVVEACHSLGVMHRDLKPNFLFDTPGEDAQMKATDFGLSVILQARQAFHDVVGSPY 191
Qy 194 VAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFRQILQGLDKSPWP 253
Db 192 VAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETAGIFRQILNGDLDFVSE 251
Qy 254 SEAAKDLIYKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAVLSELKQFSQMNK 313
Db 252 SENAKELVKQMLDRDPKKRISAHEVLCNPWVDD-IAPDKPLDSAVLTRKHFSA 310
Qy 314 KVALRVIAERLSEEEIGGLKELFKMIDTNSGTTITFEELKAGLKRVSSELSLMD 373
Db 311 KVALRVIAERLSEEEIGGLKELFKMIDTNSGTTITFEELKEGKUSVGSNLMSE 370
Qy 374 AADTNSGTTIDYGEFLAATLHNKMEREEILVAAESDPKQSGYITIDELOSACTEPGL 433
Db 371 AADTNSGTTIDYGEFLAATLHNKMEREEILVAAESDPKQSGYITIDELOQACKDFSL 430
Qy 434 CDTPLDDMIKEIDLNDGKIDFSEFTAMMRKGD-GVGRSRRTMMKNLNF 498
Db 431 GDVHLEMIKEIDQNDGRIDYAEFAAMKKGDPNMGRSRRTMMKNLNF 486
RESULT 4
A43713
calcium-dependent protein kinase (EC 2.7.1.1-) - soybean
C:Species: Glycine max (soybean)
C:Date: 03-Mar-1993 #sequence_revision 14-Jul-1994 #text_change 11-Jun-1999
C:Accession: A43713
R:Harper, J.F.; Sussman, M.R.; Schaller, G.B.; Putnam-Evans, C.; Charbonneau, H.; Harm
Science 252, 951-954, 1991
A:Title: A calcium-dependent protein kinase with a regulatory domain similar to calmod

A:Reference number: A43713; MUID:91240279; PMID:1852075

A:Accession: A43713

A:Molecule type: mRNA

A:Residues: 1-508 <HAR>

A:Cross-references: EMBL:M64987; NID:G169930; PIDN:AAB00806.1; PID:G169931

C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kinase

C:Keywords: ATP; calcium binding; EF hand; phosphotransferase; serine/threonine-specific

F:32-292/Domain: protein kinase homology <KIN>

F:40-48/Region: protein kinase ATP-binding motif

F:335-367/Domain: calmodulin repeat homology <EF1>

F:371-403/Domain: calmodulin repeat homology <EF2>

F:407-439/Domain: calmodulin repeat homology <EF3>

F:441-473/Domain: calmodulin repeat homology <EF4>

F:63/Active site: Lys #status predicted

Query Match 75.0%; Score 1944; DB 1; Length 508;

Best Local Similarity 77.7%; Pred. No. 1.6e-65;

Matches 370; Conservative 51; Mismatches 51; Indels 4; Gaps 3;

QY 14 VLPYQTPRLRDHYLLGKLGQCGQGTTLCTEKSSTANYACKSPKRLKVCREDYEDVWR 73

DB 22 VLPQRTQNIREVVEYGRKLGQCGQGTTFCTRRASGGKFPACKSPKRLCKEDYEDVWR 81

QY 74 EQIMHLSHNPVRIKGTIEDSVFVHVEVCEGGLFDRIVSKGHFSREAVKLKT 133

DB 82 EQIMHLSHNPVRIKGTIEDSVFVHVEVCEGGLFDRIVSKGHFSREAVKLKT 141

QY 134 ILGVVACHSLGVMHRLKPNFLDPSKODAKLKATDGLSVFVKPGQYLYDVVGGPY 193

DB 142 IVEVVEACHSLGVMHRLKPNFLDPTIDEDAKLKATDGLSVFVKPGESCDVVGSPY 201

QY 194 VAPVLKCYGPEIDVMSAGVILYLLSGVPPFWAETSGIFRQILQKLFKDPPTI 253

DB 202 VAPVLKCYGPEIDVMSAGVILYLLSGVPPFWAETSGIFRQILQKLFKDPPTI 261

QY 254 SEAAKLLIYKMLERSPKKISAEALCHPWIDEQAAPDKPLDPAVLRLKQFSOMKIK 313

DB 262 SDAAKLLIYKMLERSPKKISAEALCHPWIDEQAAPDKPLDPAVLRLKQFSOMKIK 321

QY 314 KMLRVIAERLSEETGGKELFKMIDTNSGTITFEELKAGLKVGSSELMSEIKSLMD 373

DB 322 KMLRVIAERLSEETGGKELFKMIDTNSGTITFEELKAGLKVGSSELMSEIKSLMD 381

QY 374 AADIDNSGTIDYGEFLAATLHNMKVEREILVAAPSDPKDQSGYITIDELQSACTEGL 433

DB 382 AADIDNSGTIDYGEFLAATLHNMKVEREILVAAPSDPKDQSGYITIDELQSACTEGL 441

QY 434 CDTPLDDMIKEIDLNDGKIDFSEFTAMVRKGD-GVGRSRTMMKLNFIADAFGV 488

DB 442 DDIHIDMIKEIQDNDGQIDYGEFAAMVRKGNNGIGR-RTWRKTL--NLRDALGL 494

RESULT 5

S71776

calcium-dependent protein kinase (EC 2.7.1.1) 9 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 14-May-1999 #sequence revision 14-May-1999 #text_change 18-Jun-1999

A:Accession: S71776; S71775; S71902; S71196

R:Hong, Y.; Takano, M.; Liu, C.M.; Gasch, A.; Chye, M.L.; Chua, N.H.

Plant Mol. Biol. 30, 1259-1275, 1996

A:Title: Expression of three members of the calcium-dependent protein kinase gene family

A:Reference number: S71774; MUID:96311013; PMID:8704134

A:Accession: S71776

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-490 <HON>

A:Cross-references: EMBL:U20626

A:Accession: S71775

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-490 <HOF>

A:Cross-references: EMBL:U20388

R:Hong, Y.; Takano, M.; Liu, C.M.; Gasch, A.; Chye, M.L.; Tan, C.T.; Koh, C.C.; Chua, N.H.

submitted to the EMBL Data Library, February 1995

A:Description: Expression of the calcium-dependent protein kinase gene family in Arabid

A:Reference number: S71197

A:Accession: S71902

A:Molecule type: DNA

A:Residues: 1-164, 'S', 166-239, 'E', 241-300, 'KF', 303-350, 'S', 352-490 <HOW>

A:Cross-references: EMBL:U20626; NID:G836945; PIDN:AAA67657.1; PID:G836946

R:Hong, Y.; Takano, M.; Liu, C.M.; Gasch, A.; Chye, M.L.; Tan, C.T.; Koh, C.C.; Chua, N

submitted to the EMBL Data Library, January 1995

A:Description: Expression of the calcium dependent protein kinase gene family in Arabid

A:Reference number: S71196

A:Accession: S71196

A:Molecule type: mRNA

A:Residues: 1-164, 'S', 166-239, 'E', 241-300, 'KF', 303-350, 'S', 352-490 <HOA>

A:Cross-references: EMBL:U20388; NID:G836937; PIDN:AAA67653.1; PID:G836938

C:Genetics:

A:Gene: CDPK9

A:Introns: 177/1; 225/1; 276/1; 370/3; 445/3

C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kin

C:Keywords: ATP; calcium binding; EF hand; phosphotransferase; serine/threonine-specific

F:20-280/Domain: protein kinase homology <KIN>

F:228-367/Region: protein kinase ATP-binding motif

F:323-355/Domain: calmodulin repeat homology <EF1>

F:359-391/Domain: calmodulin repeat homology <EF2>

F:395-427/Domain: calmodulin repeat homology <EF3>

F:429-461/Domain: calmodulin repeat homology <EF4>

F:51/Active site: Lys #status predicted

Query Match 71.2%; Score 1847.5; DB 1; Length 490;

Best Local Similarity 73.5%; Pred. No. 5.6e-62;

Matches 355; Conservative 52; Mismatches 69; Indels 7; Gaps 2;

QY 1 METKNPRPNTVLPYCTPLRDHYLLGKLGQCGQGTTLCTEKSSTANYACKSPK 60

DB 1 VANKPRTT---WVLPYKTRNVEDNYFLGVLGQCGQGTTLCTHKTGQGLACKSPK 56

QY 61 KLVCREDYEDVWREIQIMHLSHNPVRIKGTIEDSVFVHVEVCEGGLFDRIVSKG 120

DB 57 KLLCEDYEDVWREIQIMHLSHNPVRIKGTIEDSVFVHVEVCEGGLFDRIVSKG 116

QY 121 HFSEBAVKLITLGVVEACHSLGVHREDLKPNFLDPSKODAKLKATDGLSVFYKP 180

DB 117 HYSEBAVKLITVIGVVEACHSLGVHREDLKPNFLDPSKODAKLKATDGLSVFYCTP 176

QY 181 GOYLDVWVSPYVVAPEVLKCYGPEIDVMSAGVILYLLSGVPPFWAETSGIFRQILQ 240

DB 177 GFAPSELVGSAYVVAPEVLKCYGPEIDVMSAGVILYLLSGVPPFWAETSGIFRQILQ 236

QY 241 GKLDKSPDPWPTISAAKDLIYKMLERSPKKISAEALCHPWIDEQAAPDKPLDPAVL 300

DB 237 GKLDPEINPWPISBSAKDLIYKMLERSPKKISAEALCHPWIDEQAAPDKPLDPAVL 296

QY 301 SRLKQFSQWNTKKMVALRVIAERLSEETGGKELFKMIDTNSGTITFEELKAGLKV 360

DB 297 SRLKQFSQWNTKKMVALRVIAERLSEETGGKELFKMIDTNSGTITFEELKAGLKV 356

QY 361 SELMSEIKSLMDAADINSGTIDYGEFLAATLHNMKVEREILVAAPSDPKDQSGYIT 420

DB 357 SELMSEIQELLRAADVDESSTIDYGEFLAATLHNMKVEREILVAAPSDPKDQSGYIT 416

QY 421 IDELQSACTEFLGLCTPLDDMIKEIDLNDGKIDFSEFTAMVRKGDGVGRS---RTWMKN 477

DB 417 IEELQSACTEFLGLCTPLDDMIKEIDLNDGKIDFSEFTAMVRKGDGVGRS---RTWMKN 476

QY 478 LNF 480

DB 477 LNF 479

RESULT 6

T03271

calcium-dependent protein kinase (EC 2.7.1.1) 1 - maize

C:Species: Zea mays (maize)

C>Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 16-Jun-2000
 C/Accession: T03271
 R/Berberich, T.; Kusano, T.
 Mol. Gen. Genet. 254, 275-283, 1996
 A/Title: Cycloheximide induces a subset of low temperature-inducible genes in maize.
 A/Reference number: Z14873
 A/Accession: T03271
 A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-492 <BER>
 A/Cross-references: EMBL:D84408; PIDN:BAAL2338.1
 A/Experimental source: strain honey bantum
 A/Note: low temperature-inducible
 C/Genetics:
 A/Gene: CDPK1
 C/Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kinase
 C/Keywords: ATP; calcium binding; EF hand; phosphotransferase; serine/threonine-specific
 F/25-285/Domain: protein kinase homology <KIN>
 F/33-41/Region: protein kinase ATP-binding motif
 F/328-360/Domain: calmodulin repeat homology <EF1>
 F/364-396/Domain: calmodulin repeat homology <EF2>
 F/400-432/Domain: calmodulin repeat homology <EF3>
 F/434-466/Domain: calmodulin repeat homology <EF4>
 F/56/Active site: Lys #status predicted

Query Match 67.6%; Score 1752; DB 1; Length 492;
 Best Local Similarity 70.6%; Pred. No. 1.9e-58;
 Matches 334; Conservative 54; Mismatches 83; Indels 2; Gaps 2;

QY 13 TVLPYQTPRLRDHYLLGKLGOGQFGTTLCTEKSANSYACKSPKRLKVCREDYEDVW 72
 DB 14 SVLHKTPIRDLTYALGRKLGQGGTTLCTELATGIDYACKSKRLKTEDVDVR 73

QY 73 REIQMHLSSEHPNVVRIRKTYEDSVFVHVMVECGEGELFDRIVSKGHFSREAVKLK 132
 DB 74 REIQMHLSGHKNVVAIKGAYEDQVHVHVMELCAGGELFDRIIQRGHYSRKAALTR 133

QY 133 TLGVVACHSLGWHRDLKPENFLPDSKDDAKLKATDGLSVFKPGQYLYDVVGSPPY 192
 DB 134 IIVGVVACHSLGWHRDLKPENFLANRDDLSLKADFGLSVFFKPGQVTTDVVGSPPY 193

QY 193 YVAPEVLKCYGPDIWVSAGVILYLLSGVPPFPAETESGIFRQIQLOGLDFKSDPWP 252
 DB 194 YVAPEVLKSGVPAADVTAGVILYLLSGVPPFPAETQGGIFDAVLKGAIDFSDPWPV 253

QY 253 ISEAAKOLIVKQLERSPKKRISEAHLCHPWIVDEQAAPDKPLDPAVLRLKQFSOMNKI 312
 DB 254 ISDSAKOLIREMLNPRPAERLTAEVLCHPWIRDHGVAPDRPLDPAVLRLKQFSAMNKL 313

QY 313 KKMALRVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLRKRVGSELMESEIKSLM 372
 DB 314 KKMALRVIAESLSSEETAGLKEMFTWDTNSGAIYDELKGLRKVGSTLKDTEIRDL 373

QY 373 DAADIDNSGTTIDYGEFFAATLHMKNKREBELVAAPSDPKDQSGVITIDELQSACTERG 432
 DB 374 DAADIDNSGTTIDYIEFFAATLHMLKREBELVAAPSFYDKDQSGVITIDELQACKEHN 433

QY 433 LCDTPLDDMIKEIDLNDGKIDFSEFTAMMRKGD-GVGRSRMTMMKNLNFNIAD 484
 DB 434 WDAFLDDVINEADQNDGRIDYGEFVAMTKGNMGVGR-RTMNSLNLSMRD 485

RESULT 7
 S71770
 C/Species: Vigna radiata (mung bean)
 C/Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 11-Jun-1999
 A/Accession: S71770
 R/Botella, J.R.; Arteca, J.M.; Somdevilla, M.; Arteca, R.N.
 Plant Mol. Biol. 30, 1129-1137, 1996
 A/Title: Calcium-dependent protein kinase gene expression in response to physical and chemical stress in mung bean.
 A/Reference number: S71770; MUID:96311003; PMID:8704124
 A/Accession: S71770

A/Molecule type: mRNA
 A/Residues: 1-487 <BOT>
 A/Cross-references: EMBL:U08140; NID:967124; PIDN:AAC49405.1; PID:967125
 A/Experimental source: strain Rwlcz, cv. Berken, clone pV-CDPK-1
 C/Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kinase
 C/Keywords: ATP; calcium binding; EF hand; phosphotransferase; serine/threonine-specific
 F/22-282/Domain: protein kinase homology <KIN>
 F/30-38/Region: protein kinase ATP-binding motif
 F/325-357/Domain: calmodulin repeat homology <EF2>
 F/361-393/Domain: calmodulin repeat homology <EF3>
 F/397-429/Domain: calmodulin repeat homology <EF4>
 F/431-463/Domain: calmodulin repeat homology <EF5>
 F/53/Active site: Lys #status predicted

Query Match 67.5%; Score 1751; DB 1; Length 487;
 Best Local Similarity 69.1%; Pred. No. 2e-58;
 Matches 327; Conservative 64; Mismatches 80; Indels 2; Gaps 2;

QY 14 VLPYQTPRLRDHYLLGKLGOGQFGTTLCTEKSANSYACKSPKRLKVCREDYEDVW 73
 DB 12 VLGHTPIRDLTYLGRKLGQGGTTLCTENSTSNYACKSKRLKSKEDVEDVR 71

QY 74 REIQMHLSSEHPNVVRIRKTYEDSVFVHVMVECGEGELFDRIVSKGHFSREAVKLK 133
 DB 72 REIQMHLSGHKNVVAIKGAYEDQVHVHVMELCAGGELFDRIIQRGHYSRKAALTKI 131

QY 134 ILGVVACHSLGWHRDLKPENFLPDSKDDAKLKATDGLSVFKPGQYLYDVVGSPPY 193
 DB 132 IIVGVVACHSLGWHRDLKPENFLVNDKDDLSLKADFGLSVFFKPGQVTTDVVGSPPY 191

QY 194 YVAPEVLKCYGPDIWVSAGVILYLLSGVPPFPAETESGIFRQIQLOGLDFKSDPWP 253
 DB 192 YVAPEVLKHYGPADVTAGVILYLLSGVPPFPAETQGGIFDAVLKGHIDFSDPWP 251

QY 254 SEAAKOLIVKQLERSPKKRISEAHLCHPWIVDEQAAPDKPLDPAVLRLKQFSOMNKI 313
 DB 252 SDSGKDLIRKMLCSQPSERLTAHQVLCHPWICENGAPDRAIDPAVLRLKQFSAMNKL 311

QY 314 KKMALRVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLRKRVGSELMESEIKSLM 373
 DB 312 KKMALRVIAESLSSEETAGLRKEMFQADTNSGAIYDELKAGLRVGSTLKDVEIRDL 371

QY 374 DAADIDNSGTTIDYGEFFAATLHMKNKREBELVAAPSDPKDQSGVITIDELQSACTERG 433
 DB 372 AADVXSGTTIDYGEFFAATLHMLKREBELVAAPSFYDKDQSGVITIDELQACAEHNM 431

QY 434 CDTPLDDMIKEIDLNDGKIDFSEFTAMMRKGD-GVGRSRMTMMKNLNFNIAD 485
 DB 432 TDAFLDDVINEADQNDGRIDYGEFVAMTKGNMGVGR-RTMNSLNLSMRD 483

RESULT 8
 T03263
 C/Species: Zea mays (maize)
 C/Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000
 C/Accession: T03263
 R/Saijo, Y.; Hata, S.; Sheen, J.; Izui, K.
 Biochim. Biophys. Acta 1350, 109-114, 1997
 A/Title: CDNA cloning and prokaryotic expression of a maize calcium-dependent protein kinase
 A/Reference number: Z14815; MUID:97201047; PMID:9048876
 A/Accession: T03263
 A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-554 <SAI>
 A/Cross-references: EMBL:D87042; NID:91504051; PIDN:BAAL3232.1; PID:91504052
 A/Experimental source: strain inbred line H84, clone CDPK7
 C/Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kinase
 C/Keywords: ATP; calcium binding; EF hand; phosphotransferase; serine/threonine-specific
 F/89-345/Domain: protein kinase homology <KIN>
 F/197-105/Region: protein kinase ATP-binding motif
 F/392-424/Domain: calmodulin repeat homology <EF1>
 F/428-460/Domain: calmodulin repeat homology <EF2>

F;464-496/Domain: calmodulin repeat homology <EF3>
F;498-530/Domain: calmodulin repeat homology <EF4>
F;120/Active site: Lys #status Predicted

Query Match 67.3%; Score 1745; DB 1; Length 554;
Best Local Similarity 70.0%; Pred. No. 3.8e-58;
Matches 333; Conservative 57; Mismatches 84; Indels 2; Gaps 2;

QY 13 TVLPYQTPRLRDHYLLGKLGQGGQFGTTLCTEKSSTANYACKSIPKRLKVCREDYEDVW 72
DB SVLGHTPTNRLDLYALGKLGQGGQFGTTLCTELATGVDYACKSISKRLITREDVDVVR 137
QY 73 REIQIMHLSHPNVVRIKGTIEDSVFVHIVMEVCEGGELEFDRIVSKGHFSERAVKLIK 132
DB 138 REIQIMHLSGHTNVVAIKGAYEDQLYVHIVMELCAGGELEFDRIIQRGHYSERKAAELTR 197
QY 133 TIIGVVEACHSLGWHRDLKPNFLFDSKDDAKLKATDFGLSVFKPGQYLYDVVGSPP 192
DB 198 IIVGVVEACHSLGWHRDLKPNFLVKNDDLSLKADFGLSVFKPGQVFTDVVGSPP 257
QY 193 YVAPVILKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFRQILQGLKDF 252
DB 258 YVAPVILKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFRQILQGLKDF 317
QY 253 ISPAKDLIYMLERSPKKRI SAHEALCHPWIVDEQAAPDKPLDPAVLRLKQFSQNNKI 312
DB 318 ISPAKDLIYMLERSPKKRI SAHEALCHPWIVDEQAAPDKPLDPAVLRLKQFSQNNKI 377
QY 313 KQVALRVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLRVSGELMESIKSLM 372
DB 378 KQVALRVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLRVSGELMESIKSLM 437
QY 373 DAADINSGTIDYGEFLAATLHMVREELVAAPSDPKDGSVITIDELQSACTEFG 432
DB 438 DAADINSGTIDYGEFLAATLHMVREELVAAPSDPKDGSVITIDELQSACTEFG 497
QY 433 LCDTPDDMIKEIDLNDGKIDFSEFTAMVRKGD-GVGRSRTMMKLNFNFIADAF 487
DB 498 MPDAFLDDVINEADQNDGRIDYGEFVAMTKGNMGVGR-RTMNSLNISMMDAPG 552
RESULT 9
T06126
calcium-dependent protein kinase (EC 2.7.1.-) CPK5 - Arabidopsis thaliana
N;Alternate names: Protein F23E12.130
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 21-Jan-2000
R;Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Hohnsels,
submitted to the Protein Sequence Database, April 1999
A;Reference number: Z15485
A;Accession: T06126
A;Molecule type: DNA
A;Residues: 1-556 <BEV>
A;Cross-references: EMBL:AL022604; GSPDB:GN00062; ATSP:F23E12.130
A;Experimental source: cultivar Columbia; BAC clone F23E12
C;Genetics:
A;Gene: CPK5; ATSP:F23E12.130
A;Map position: 4
A;Introns: 252/1; 300/1; 351/1; 389/3; 445/3; 520/3
C;Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kinase
C;Keywords: EF hand; phosphotransferase; protein kinase
F;93-355/Domain: protein kinase homology <KIN>
F;398-430/Domain: calmodulin repeat homology <EF1>
F;434-466/Domain: calmodulin repeat homology <EF2>
F;470-502/Domain: calmodulin repeat homology <EF3>
F;504-536/Domain: calmodulin repeat homology <EF4>

Query Match 67.2%; Score 1742; DB 2; Length 556;
Best Local Similarity 68.4%; Pred. No. 4.9e-58;
Matches 329; Conservative 66; Mismatches 84; Indels 2; Gaps 2;

QY 6 NPPRDSNTVLPYQTPRLRDHYLLGKLGQGGQFGTTLCTEKSSTANYACKSIPKRLKVC 65

DB 77 NPDNQAYVVLGHKTPNRIIDYTLRSKLGQGGQFGTTLCTEKSSTANYACKSIPKRLKISK 136
QY 66 EDYEDVMEIRIQIMHLSHPNVVRIKGTIEDSVFVHIVMEVCEGGELEFDRIVSKGHFSE 125
DB 137 EDYEDVMEIRIQIMHLSHPNVVRIKGTIEDSVFVHIVMEVCEGGELEFDRIVSKGHFSE 196
QY 126 EAVKLIKTIIGVVEACHSLGWHRDLKPNFLFDSKDDAKLKATDFGLSVFKPGQYLY 185
DB 197 KAAELTKIIGVVEACHSLGWHRDLKPNFLVKNDDLSLKADFGLSVFKPGQVFTDVVGS 256
QY 186 DVVGSPPYVAPSVILKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFRQILQGLKDF 245
DB 257 DVVGSPPYVAPSVILKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFRQILQGLKDF 316
QY 246 KSDPPTTSEAAKDLIYMLERSPKKRI SAHEALCHPWIVDEQAAPDKPLDPAVLRLKQ 305
DB 317 ESDPPTTSEAAKDLIYMLERSPKKRI SAHEALCHPWIVDEQAAPDKPLDPAVLRLKQ 376
QY 306 FSOINKIKQVALRVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLRVSGELME 365
DB 377 FSOINKIKQVALRVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLRVSGELME 436
QY 366 SEIKSLMDAADINSGTIDYGEFLAATLHMVREELVAAPSDPKDGSVITIDELQ 425
DB 437 TEIHDLMDAADINSGTIDYGEFLAATLHMVREELVAAPSDPKDGSVITIDELQ 496
QY 426 SACTEFGLCDTPDDMIKEIDLNDGKIDFSEFTAMVRKGD-GVGRSRTMMKLNFNFIAD 484
DB 497 QACVBEHGMADVLEDIIKEVDQNDGKIDYGEFVEMVQKGNAGVGR-RTMNSLNISM 555
QY 485 A 485
DB 556 A 556

RESULT 10

DB4550
probable calmodulin-domain protein kinase CPK6 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Mar-2001
C;Accession: D84550
M.; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Varkken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, A.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: D84550
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-544 <STO>
A;Cross-references: GB:AE002093; NID:G2623752; PIDN:AAB86506.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g17290
A;Map position: 2
C;Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein ki
C;Keywords: EF hand

Query Match 66.8%; Score 1731; DB 2; Length 544;
Best Local Similarity 68.3%; Pred. No. 1.2e-57;
Matches 328; Conservative 65; Mismatches 85; Indels 2; Gaps 2;

QY 6 NPPRDSNTVLPYQTPRLRDHYLLGKLGQGGQFGTTLCTEKSSTANYACKSIPKRLKVC 65

DB 65 NVNQSYVVLGHKTPNRIIDYTLRSKLGQGGQFGTTLCTEKSSTANYACKSIPKRLKISK 124

QY 66 EDYEDVMEIRIQIMHLSHPNVVRIKGTIEDSVFVHIVMEVCEGGELEFDRIVSKGHFSE 125

DB 125 EDYEDVMEIRIQIMHLSHPNVVRIKGTIEDSVFVHIVMEVCEGGELEFDRIVSKGHFSE 184

QY 126 EAVKLIKTIIGVVEACHSLGWHRDLKPNFLFDSKDDAKLKATDFGLSVFKPGQYLY 185

Db 185 KAALTKIIVGVVEACHSLGVNHRDLKPNFLLNVKDDFSLKAIDFGLSVFFKPGQIFK 244
 QY 186 DVVSGSVYVAPELVKCYGPEIDVNSAGVILYLLSGVPPFWAETESGIFROILOGLKDF 245
 Db 245 DVVSGSVYVAPELVKCYGPEIDVNSAGVILYLLSGVPPFWAETESGIFROILOGLKDF 304
 QY 246 KSPFWPTISEAAKDLIYKMLERSPKKRISAHEALCHPWVDEQAAPKPDPAVLSRLKQ 305
 Db 305 DTPFWPVIDSADKDLIRKMLCSPPSERLTAHEVLRHPWICENGAVPADRALDPAVLSRLKQ 364
 QY 306 FSONKIKOMALRVIAERLSSEIEIGLKFMDITDNGSGITTFEELKAGLRKRVGSELM 365
 Db 365 FSAWKLKXKALVIAERLSSEIEIGLKFMDITDNGSGITTFEELKAGLRKRVGSELM 424
 QY 366 SEIKSMDAADINDSGTIDYGFELATLHMKNKREBEILLVAAPDFDKDGSYITIDELQ 425
 Db 425 TEIRDLEAADVNSGTIDYSEFIAATHLNKLEHEHLVSAFYQFDKDGSGYITIDELQ 484
 QY 426 SACTEFLGCDTLPDDMIKEIDLNDGKIDFSEFTAMRKGD-GVGRSRTMMKNLNFIAD 484
 Db 485 QSCIEHGMTDVFLEIDIEKVDQDNDGRIDYEFVAMQKGNAGVR-RTMKNLSINISMRD 543
 RESULT 11
 A49082
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 11-Jun-1999
 C:Accession: A49082
 R:Harper, J.F.; Binder, B.M.; Sussman, M.R.
 Biochemistry 32, 3282-3290, 1993
 A:Title: Calcium and lipid regulation of an Arabidopsis protein kinase expressed in Esch
 A:Reference number: A49082; NCBI:93213795; PMID:7916621
 A:Contents: ecotype Columbia
 A:Accession: A49082
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-610 <HR>
 A:Cross-references: GB:14771; MID:9289189; PIDN:AAA32761.1; PID:G304105
 A:Note: sequence extracted from NCB1 backbone (NCB1:128903, NCBIP:128904)
 C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kin
 C:Keywords: ATP; calcium binding; EF hand; phosphotransferase; serine/threonine-specific
 F:148-408/Domain: protein kinase homology <KIN>
 F:156-164/Region: protein kinase ATP-binding motif
 F:451-483/Domain: calmodulin repeat homology <EF1>
 F:487-519/Domain: calmodulin repeat homology <EF2>
 F:523-555/Domain: calmodulin repeat homology <EF3>
 F:557-589/Domain: calmodulin repeat homology <EF4>
 F:179/Active site: Lys #status predicted

QY 282 PWIVDEQAAPKPDPAVLSRLKQFSONKIKOMALRVIAERLSSEIEIGLKFMDIT 341
 Db 406 PWVQVGVAPDFLDSAVLSRMKQFSAMNKKOMALRVIAERLSSEIEIGLKFMDIT 465
 QY 342 DNGSGITTFEELKAGLRKRVGSELMSEIEISLMDAADINDSGTIDYGEFLATLHMKNKRE 401
 Db 466 DKSGQITTFEELKAGLRKRVGSELMSEIEISLMDAADINDSGTIDYGEFLATLHMKNKRE 525
 QY 402 EILVAFAFDFDKDGSYITIDELQSACTEFLGCDTLPDDMIKEIDLNDGKIDFSEFTAM 461
 Db 526 DHLFAAFTYFDKDGSGYITIDELQSACTEFLGCDTLPDDMIKEIDLNDGKIDFSEFTAM 585
 QY 462 MRKGDGVGRSRTMMKNLNFIAD 483
 Db 586 MQKSGITGGPVVQGLEKSFSLA 607
 RESULT 12
 T09940
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
 C:Accession: T09940
 R:Billard-ivey, M.; Hopkins, R.B.; White, T.J.; Lomax, T.L.
 Plant Mol. Biol. 39, 199-208, 1999
 A:Title: Cloning, expression and N-terminal myristoylation of CpcPK1, a calcium-depende
 A:Reference number: Z16898; MUID:99178773; PMID:10080688
 A:Accession: T09940
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-573 <ELL>
 A:Cross-references: EMBL:U90262; NID:91899174; PIDN:AAB49984.1; PID:g1899175
 A:Experimental source: etiolated hypocotyls
 C:Genetics:
 A:Gene: CPK1
 C:Function:
 A:Description: serine/threonine-specific protein kinase activated by direct binding of
 C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein ki
 C:Keywords: ATP; calcium binding; EF hand; membrane protein; myristylation; phosphotrar
 F:108-368/Domain: protein kinase homology <KIN>
 F:447-479/Domain: calmodulin repeat homology <EFH>
 Query Match 65.9%; Score 1709.5; DB 2; Length 573;
 Best Local Similarity 64.8%; Pred. No. 8e-57;
 Matches 321; Conservative 78; Mismatches 79; Indels 17; Gaps 3;
 QY 4 KNPDR-----RP-----SNTVLPYQTPRLRDHYLLGKLGQGGQFGTTVLCCTEKS 47
 Db 72 KPPEPMPKVRPYMKRVGSAGLRGGSVLQTKTGNFKYISLGKLGQGGQFGTTVCMVEKA 131
 QY 48 TSANYACKSIPTKELVCREDEYDVMREIQIMHLSHHPNVRIRKTYEDSVFVHVMVEVC 107
 Db 132 TGKEYACKSIPTKELVCREDEYDVMREIQIMHLSHHPNVRIRKTYEDSVFVHVMVEVC 191
 QY 108 EGGELPRLIVSKGHFEREAVKLIKTILGVBEACHSLGVNHRDLKPNFLDPSKDAKL 167
 Db 192 AGGELFRLIQRGHYTERKAAELTRIVGVLEACHSLGVNHRDLKPNFLDPSKDAKL 251
 QY 168 KATDFGLSVFYKPGQVLYDVVSGSVYVAPELVKCYGPEIDVNSAGVILYLLSGVPPFW 227
 Db 252 KTIDFGLSMFVKPGKXFNVDVSGSVYVAPELVKCYGPEIDVNSAGVILYLLSGVPPFW 311
 QY 228 AETESGIFROILOGLKDFKSDNPWTISEAAKDLIYKMLERSPKKRISAHEALCHPWVDE 287
 Db 312 AESSEGFIEFVLEHGLDFFSDPWPFSISDSAKDLVRRMLVRDPKELTAYELVCHPWVQVD 371
 QY 288 QAAPKPDPAVLSRLKQFSONKIKOMALRVIAERLSSEIEIGLKFMDITDNGSGIT 347
 Db 372 GVA PDKELDSAVLTLKQFSAMNKKOMALRVIAERLSSEIEIGLKFMDITDNGSGIT 431
 QY 348 TFEELKAGLRKRVGSELMSEIEISLMDAADINDSGTIDYGEFLATLHMKNKREBEILVAA 407

Db 432 TFEELKAGLKFGANKSEIYDLMOADIINNGTIDYGEFVAATLHNLKIEKEDHLLAA 491
Qy 408 FSDFDKDGSGYITIDELQSACTEFGCLCTDIDMIKEIDLDNDGKIDFSEFTAMMRKGDGVGRSRTMMKNLNFNI 482
Db 492 PSYFDKDGSGFITHDELQCAKKEFGIEDLQWENREVDQNDGSDIDYNEFVAMQKGNV 551
Qy 468 VGRSRTMMKNLNFNI 482
Db 552 VNTGKGLQS-SFSI 565

RESULT 13
T02650
calcium-dependent protein kinase (EC 2.7.1.1) - Arabidopsis thaliana
N;Alternate names: protein F20D10.350
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 21-Jan-2000
C;Accession: T05650
R;Revan, M.; Wedler, H.; Kutner, M.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.
submitted to the Protein Sequence Database, February 1999
A;Reference number: Z15420
A;Accession: T05650
A;Molecule type: DNA
A;Note: F20D10.350
A;Residues: 1-484 <BEV>
A;Cross-references: EMBL:AL035538
A;Experimental source: cultivar Columbia; BAC clone F20D10
C;Genetics:
A;Map position: 4
A;Intons: 179/1; 227/1; 278/1; 316/3; 372/3; 447/3
A;Note: F20D10.350
C;Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kin
C;Keywords: ATP; calcium binding; EF hand; phosphotransferase; serine/threonine-specific
F;22-282/Domain: protein kinase homology <KIN>
F;30-38/Region: protein kinase ATP-binding motif
F;325-357/Domain: calmodulin repeat homology <EF1>
F;361-393/Domain: calmodulin repeat homology <EF2>
F;397-429/Domain: calmodulin repeat homology <EF3>
F;431-463/Domain: calmodulin repeat homology <EF4>
F;53/Active site: Lys #status predicted

Query Match 65.6%; Score 1700.5; DB 2; Length 484;
Best Local Similarity 69.3%; Pred. No. 1.5e-56;
Matches 325; Conservative 60; Mismatches 81; Indels 3; Gaps 2;

Qy 14 VLPYQTPRLRDHYLLGKLGQGGFGTTLCTEKTSTANSYACKSIPRKLVCREDYEDVWR 73
Db 12 VLQGTPTSIDLYSLGKLGQGGFGTTLCTEKTSTANSYACKSIPRKLVCREDYEDVWR 71
Qy 74 EIQIMHLSHPNVRIKGYEDSVFVHIVMEYCEGELFDRIIVSKGHFSEAEVKLIKT 133
Db 72 EIQIMHLSHPNVRIKGYEDSVFVHIVMEYCEGELFDRIIVSKGHFSEAEVKLIKT 131
Qy 134 ILGVVEACHSLGVNHRDLKPENFLFSDPKDDAKLKATDFGLSVFYKPGQYLDVVGSPY 193
Db 132 IVGVVEACHSLGVNHRDLKPENFLVNNKDDFSLKAIDFGLSVFYKPGQYLDVVGSPY 191
Qy 194 VAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFQILQGLDKPSDWPPI 253
Db 192 VAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFQILQGLDKPSDWPPI 251
Qy 254 SEAAKDIYKMLERSPKKRISAHEALCHPWIIVDEQAPDPAVLRLKQFSQMNKIK 313
Db 252 SDSAKNLRGMCLSRPSERLTAHQVLRHPICENGAVPADRALDPAVLRLKQFSQMNKIK 311
Qy 314 KOALRVIAERLSEIEIGLKLKELFKVITDINSGITTFEELKAGIKRVGSELSMSEIKSLND 373
Db 312 QMALRVIAERLSEIEIGLKLKELFKVITDINSGITTFEELKAGIKRVGSELSMSEIKSLND 371
Qy 374 AADINDNSTIDYGEFLAATLHNMKWEREILVAAFSDFDKDGGSYITIDELQSACTEFGCL 433
Db 372 AADINDNSTIDYGEFLAATLHNMKWEREILVAAFSDFDKDGGSYITIDELQSACTEFGCL 431

Qy 434 CDTPLDDMIKEIDLDNDGKIDFSEFTAMMRKGDGVGRSRTMMKNLNFNI 482
Db 432 SDVFEEDVIKEVDQNDGRIIDYGEFVAMQKGI-VG--RTMRKSINMSI 477

RESULT 14
T02784
calcium-dependent protein kinase (EC 2.7.1.1) - maize (strain W64A)
C;Species: Zea mays (maize)
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 16-Jun-2000
C;Accession: T02784
R;Muriillo, I.; Jaack, E.; Cordero, M.; San Segundo, B.
submitted to the EMBL Data Library, July 1998
A;Description: A calcium-dependent protein kinase possibly involved in pathogen defense
sis-related PRms gene.
A;Reference number: Z14736
A;Accession: T02784
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-639 <MUR>
A;Cross-references: EMBL:AJ007366; PIDN:CAA07481.1
A;Experimental source: strain W64A; seed
C;Function:
A;Description: probably involved in pathogen defense in maize plants
C;Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kin
C;Keywords: ATP; calcium binding; EF hand; phosphotransferase; serine/threonine-specific
F;151-411/Domain: protein kinase homology <KIN>
F;159-167/Region: protein kinase ATP-binding motif
F;454-486/Domain: calmodulin repeat homology <EF1>
F;490-522/Domain: calmodulin repeat homology <EF2>
F;526-558/Domain: calmodulin repeat homology <EF3>
F;560-592/Domain: calmodulin repeat homology <EF4>
F;182/Active site: Lys #status predicted

Query Match 64.5%; Score 1672.5; DB 1; Length 639;
Best Local Similarity 66.2%; Pred. No. 2e-55;
Matches 318; Conservative 66; Mismatches 83; Indels 13; Gaps 3;

Qy 5 FNPRLRPS-----NTVLPYQTPRLRDHYLLGKLGQGGFGTTLCTEKTSTANSY 52
Db 120 PSRPPRPQVRYSSAGLLGLSVLRRTENLKDYSGLRRLGQGGFGTTLCTEKTSTANSY 179
Qy 53 ACKSIPRKLVCREDYEDVWRVREIQIMHLSHPNVRIKGYEDSVFVHIVMEYCEGEL 112
Db 180 ACKSILKRLGSDDDVEDVRRVREIQIMHLSHPNVRIKGYEDSVFVHIVMEYCEGEL 239
Qy 113 FDRIVSKGHFSEAEVKLIKTILGVVEACHSLGVNHRDLKPENFLFSDPKDDAKLKATDF 172
Db 240 FDRIVARGHYTERKAELARVIVGVVEACHSGVNVHRDLKPENFLFADHSEERALKTIDF 299
Qy 173 GLSVFYKPGQYLDVVGSPYVAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETES 232
Db 300 GLSIFPRPGQIFTDVVGSPYVAPEVLKCYGPEADVNSAGVILYLLCGVPPFWAENEQ 359
Qy 233 GIFRQILQGLDKPSDWPPISEAAKDIYKMLERSPKKRISAHEALCHPWIIVDEQAPD 292
Db 360 GIFEEVLHGRDLFSESEPNFSISDGAOLVRRMLVDRPKRLTAHEVLRHPVQVGGVAPD 419
Qy 293 KPDLPAVLRLKQFSQMNKIKKOALRVIAERLSEIEIGLKLKELFKVITDINSGITTFEEL 352
Db 420 RPLDSAVLSRKQFSQMNKIKKOALRVIAERLSEIEIGLKLKELFKVITDINSGITTFEEL 479
Qy 353 KAGIKRVGSELSMSEIKSLND AADINDNSTIDYGEFLAATLHNMKWEREILVAAFSDFD 412
Db 480 KVGLEKVGANLQSEIYALMQAADVNNGTIDYGEFLAATLHNMKWEREILVAAFSDFD 539
Qy 413 KDGSYITIDELQSACTEFGCLCTDIDMIKEIDLDNDGKIDFSEFTAMMRKGDGVGRS 472
Db 540 KDGSYITIDELQSACTEFGCLCTDIDMIKEIDLDNDGKIDFSEFTAMMRKGDGVGRS 598

RESULT 15
H84810

Search completed: February 13, 2003, 21:11:31
Job time : 39 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 13, 2003, 21:06:32 ; Search time 20 Seconds
(without alignments)
1026.539 Million cell updates/sec

Title: US-09-848-806-1
Perfect score: 2593
Sequence: 1 METKPNRRRSNTVLPYQTP.....KNLNENIADAFGVDGKSD 495

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1944	75.0	508	1	CDPK_SOYEN
2	1724	66.5	610	1	CDP1_ARATH
3	1586	61.2	542	1	CDP3_ORYSA
4	1482	57.2	533	1	CDP2_ORYSA
5	1460.5	56.3	513	1	CDP2_WAIZE
6	1460	56.3	513	1	CDP1_ORYSA
7	1432.5	55.2	532	1	CDPK_DAUCA
8	854	32.9	602	1	CRK_DAUCA
9	591	22.8	499	1	KCCD_HUMAN
10	589.5	22.7	374	1	KCC1_RAT
11	587.5	22.7	370	1	KCC1_HUMAN
12	578.5	22.3	473	1	KCC4_HUMAN
13	574.5	22.2	533	1	KCCD_RAT
14	574	22.1	469	1	KCC4_MOUSE
15	572	22.1	474	1	KCC4_RAT
16	571.5	22.0	542	1	KCCB_MOUSE
17	569.5	22.0	542	1	KCCB_RAT
18	567.5	21.9	478	1	KCCB_HUMAN
19	566.5	21.8	664	1	KCCB_HUMAN
20	563.5	21.7	478	1	KCCA_RAT
21	549.5	21.2	478	1	KCCA_MOUSE
22	544.5	21.0	529	1	KCCG_MOUSE
23	543.5	21.0	472	1	KCCG_HUMAN
24	539	20.8	527	1	KCCG_RAT
25	534.5	20.6	424	1	KPSI_HUMAN
26	533.5	20.6	386	1	KPBG_HUMAN
27	532.5	20.5	386	1	KPBG_RABIT
28	526	20.3	387	1	KPBG_RAT
29	524.5	20.2	387	1	KPBG_MOUSE
30	514.5	19.8	295	1	KMLC_DICDI
31	509	19.6	1431	1	DAPK_HUMAN
32	505	19.5	433	1	DKK1_RAT
33	505	19.5	740	1	DKK1_HUMAN

34	505	19.5	756	1	DKK1_MOUSE
35	499	19.2	335	1	KCC1_SCHPO
36	489.5	18.9	732	1	K6AA_CHICK
37	486	18.7	735	1	K6A1_RAT
38	484.5	18.7	512	1	K110_ARATH
39	482.5	18.6	733	1	K6A2_HUMAN
40	481	18.5	724	1	K6A1_MOUSE
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42	479	18.5	546	1	CHK2_MOUSE
43	477	18.4	733	1	K6AA_XENLA
44	476.5	18.4	733	1	K6A2_MOUSE
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RESULT 1

CDPK_SOYEN	STANDARD;	PRT;	508 AA.
ID	CDPK_SOYEN		
AC	P28583;		
DT	01-DEC-1992 (Rel. 24, Created)		
DT	01-DEC-1992 (Rel. 24, Last sequence update)		
DT	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	Calcium-dependent protein kinase SK5 (EC 2.7.1.1-) (CDPK).		
OS	Glycine max (Soybean).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;		
OC	eurosid I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.		
OX	NCBI_TaxID=3847;		
RN	[1]_TaxID=3847;		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=cv. Williams;		
RX	MEDLINE=91240279; PubMed=1852075;		
RA	Harper J.F., Suesman M.R., Schaller G.E., Putnam-Evans C.,		
RA	Chatbonneau H., Harmon A.C.;		
RT	"A calcium-dependent protein kinase with a regulatory domain similar		
RT	to calmodulin."		
RL	Science 252:951-954 (1991)		
CC	FUNCTION: MAY PLAY A ROLE IN SIGNAL TRANSDUCTION PATHWAYS THAT		
CC	INVOLVE CALCULUM AS A SECOND MESSENGER.		
CC	ENZYME REGULATION: ACTIVATED BY CALCIUM. AUTOPHOSPHORYLATION MAY		
CC	PLAY AN IMPORTANT ROLE IN THE REGULATION OF THE KINASE ACTIVITY.		
CC	TISSUE SPECIFICITY: FOUND THROUGHOUT THE PLANT.		
CC	MISCELLANEOUS: THERE ARE MULTIPLE CDPK ISOFORMS IN SOYBEAN.		
CC	SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.		
CC	CAMK SUBFAMILY.		
CC	SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -		
CC	the European Bioinformatics Institute. There are no restrictions on its		
CC	use by non-profit institutions as long as its content is in no way		
CC	modified and this statement is not removed. Usage by and for commercial		
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/		
CC	or send an email to license@isb-sib.ch).		
CC	EMBL; M64987; AAB00806.1; .		
DR	PIR; A43713; A43713.		
DR	HSP; Q3450; 1A06.		
DR	InterPro; IPR002048; EF-hand.		
DR	InterPro; IPR000719; Euk_pkinase.		
DR	InterPro; IPR002290; Ser_thr_pkinase.		
DR	Pfam; PF00036; ehand; 4.		
DR	Pfam; PF00069; pkinase; 1.		
DR	ProDom; PD000001; Euk_pkinase; 1.		
DR	ProDom; PD000012; EF-hand; 2.		
DR	SMART; SM00054; Efh; 4.		
DR	SMART; SM00220; S_TKC; 1.		
DR	PROSITE; PS00018; EF_HAND; 4.		
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.		
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.		
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.		

ALIGNMENTS

Db 286 HEDSLKTTDFGLSMFFKDPDFTDVVGSPPYVAPEVLRKRYGDEADWWSAGVIVYLLS 345
Qy 222 GVPFPAETESGIFRQILGKLDKDPWPTISEAKDLIYKMLERSPKRISAEALCH 281
Db 346 GVPFPAETEQGIFRQVLHGLDFSSDWPSTSESADLVKRLVRDPKRLTAHVQLCH 405
Qy 282 PWTVDQAPDKPLDPAVLRLKQFSQNNKIKQVALRVIAERLSEEEIGGKELFKMIDT 341
Db 406 PWQVDGVAPDKPLDPAVLRLKQFSQNNKIKQVALRVIAERLSEEEIGGKELFKMIDT 465
Qy 342 DMSGTITFELKAGLRKVGSELMSEIEKSLMDAADINDSGTIDYGEFLAATLHMVQERE 401
Db 466 DKSGQITFELKAGLRKVGSELMSEIEKSLMDAADINDSGTIDYGEFLAATLHMVQERE 525
Qy 402 EILVAAPSDPKDGGGYITIDELQACTEFGCLDPLDDMIKEIDLNDGKIDSEETAM 461
Db 526 DHLFAATYFDKGGGYITIDELQACTEFGCLDPLDDMIKEIDLNDGKIDSEETAM 585
Qy 462 MRKGDGVGRSRTMMKLNFNIA 483
Db 586 MQKSGITGGPVKXLEKSPSIA 607
RESULT 3
CDP3_ORYSA
ID CDP3_ORYSA STANDARD; PRT; 542 AA.
AC P53684;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Calcium-dependent protein kinase, isoform 1 (EC 2.7.1.-) (CDPK 11).
GN CPK11.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=cv. Arborio; TISSUE=coleoptile;
RX MEDLINE=95284352; PubMed=7766885;
RA Breviario D., Morello L., Gianni S.;
RT "Molecular cloning of two novel rice cDNA sequences encoding putative
calcium-dependent protein kinases."
RL Plant Mol. Biol. 27:953-967(1995).
CC -!- FUNCTION: MAY PLAY A ROLE IN SIGNAL TRANSDUCTION PATHWAYS THAT
INVOLVE CALCIUM AS A SECOND MESSENGER.
CC -!- ENZYME REGULATION: ACTIVATED BY CALCIUM (BY SIMILARITY).
CC -!- MISCELLANEOUS: THERE ARE MULTIPLE CDPK ISOFORMS IN RICE.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CAMK SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS. THREE OF
THEM SEEM TO BE NON FUNCTIONAL.

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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

CC EMBL; X81393; CAA57156.1; -.
DR HSP: O63450; 1A05.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00036; ehand; 4.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 1.
DR ProDom; PD000012; EF-hand; 1.
DR SMART; SM00054; EF-hand; 3.
DR SMART; SM00220; S_Tkc; 1.

DR PROSITE; PS00018; EF_HAND; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Calcium-binding; Phosphorylation; Multigene family.
FT DOMAIN 79
FT NP_BIND 81 89 ATP (BY SIMILARITY).
FT BINDING 107 107 ATP (BY SIMILARITY).
FT ACT_SITE 202 202 BY SIMILARITY.
FT DOMAIN 393 404 ANCESTRAL CALCIUM SITE 1 (POTENTIAL).
FT DOMAIN 429 440 ANCESTRAL CALCIUM SITE 2 (POTENTIAL).
FT DOMAIN 465 476 ANCESTRAL CALCIUM SITE 3 (POTENTIAL).
FT CA_BIND 499 510 EF-HAND 4 (POTENTIAL).
SQ SEQUENCE 542 AA; 61166 MW; D4D25275C126DDA CRC64;
Query Match 61.28; Score 1586; DB 1; Length 542;
Best Local Similarity 63.9%; Pred. No. 1.5e-72;
Matches 304; Conservative 68; Mismatches 102; Indels 2; Gaps 2;
Qy 11 SNTVLPTPLRDHYLLGKLGQGFQTTLYCTEKSANYACKSIPKRLVCREDYED 70
Db 64 SINVLGRKTADLRHHYIIGRKLGOAQFGTTLCTEINTGCEYACKTIPKRLTKEDVED 123
Qy 71 VVREIQIMHLSHPNPVRIKGYEDSVFHHVNEVCEGSELFDRIVSKGHFSEBAVKL 130
Db 124 VVREIQIMHLSGHNNVVAIKDVEDQAVHVMELCAGGELFDRIQERGHYSEKAAEL 183
Qy 131 IKTLGVVEACHSLQVHRDLKPNFLFDSPKDAKATKATDFGLSVFYKPGQYLYDVVGS 190
Db 184 TRIIVSIAMCHSLGWHRDLPENFLLDKDDLSIKATDFGLSVFYKPGQVFTLVGS 243
Qy 191 PYVAPEVLKCYGPEIDVWSAGVILYLSGVPPFWAETESGIFRQILGKLDKFSDDPW 250
Db 244 PYVAPEVLKRYGPESDWSAGVILYLSGVPPFWAETQGGIFDVLKGHIDFQSDPW 303
Qy 251 PTISAANKDLIVKMLERSPKRISAEALCHPWTVDVSOAAPDKPLDPAVLRLKQFSQNN 310
Db 304 PAISDAKDLIRKMLSHCPSERLKAEHLRHPWICENGVAIDQALDPSVLRKQFSQNN 363
Qy 311 KIKKVALRVIAERLSEEEIGGKELFKMIDTNSGTTTFELKAGLRKVGSELMSEIEKS 370
Db 364 KUKLALRVIAERLSEEEIGGKELFKMIDTNSGTTTFELKAGLRKVGSELMSEIEKS 423
Qy 371 LMDAADINDSGTIDYGEFLAATLHMVQEREILVAAPSDPKDGGGYITIDELQSACTE 430
Db 424 IMEAHNNVNTVHTEEFIAATLPLNKIEREHLAAFTYFDKGGGYITIDELQSACTE 483
Qy 431 FGLCDTPLDDMIKEIDLNDGKIDSEETAMMRKGDGVGRS-RTMMKLNFNIA 485
Db 484 HNMDLSLEELISEVDQNDGQIDVAEPVAMW-QGSNVLGQWQWESSLNVALRDA 538
RESULT 4
CDP2_ORYSA
ID CDP2_ORYSA STANDARD; PRT; 533 AA.
AC P53683;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Calcium-dependent protein kinase, isoform 2 (EC 2.7.1.-) (CDPK 2).
GN CPK2.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=cv. Arborio; TISSUE=coleoptile;
RX MEDLINE=95284352; PubMed=7766885;
RA Breviario D., Morello L., Gianni S.;
RT "Molecular cloning of two novel rice cDNA sequences encoding putative
calcium-dependent protein kinases."
RL

```

RL Plant Mol. Biol. 27:953-967(1995).
CC -1- FUNCTION: MAY PLAY A ROLE IN SIGNAL TRANSDUCTION PATHWAYS THAT
CC INVOLVE CALCIUM AS A SECOND MESSENGER.
CC -1- ENZYME REGULATION: ACTIVATED BY CALCIUM (BY SIMILARITY).
CC -1- MISCELLANEOUS: THERE ARE MULTIPLE CDPK ISOFORMS IN RICE.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CAMK SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR HSP; X81394; CAA57157.1; -.
DR HSP; Q63450; IA06.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00036; ehand; 4.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 1.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 4.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00018; EF HAND; 4.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR Transferrase; Serine/threonine-protein kinase; ATP-binding;
KW Calcium-binding; Phosphorylation; Multigene family.
KW DOMAIN 85 343
FT NP_BIND 91 99 ATP (BY SIMILARITY).
FT BINDING 114 114 ATP (BY SIMILARITY).
FT ACT_SITE 209 209 BY SIMILARITY.
FT CA_BIND 398 409 EF-HAND 1 (POTENTIAL).
FT CA_BIND 434 445 EF-HAND 2 (POTENTIAL).
FT CA_BIND 470 481 EF-HAND 3 (POTENTIAL).
FT CA_BIND 505 516 EF-HAND 4 (POTENTIAL).
SQ SEQUENCE 533 AA; 59522 MW; DOBC570ABD289E28 CRC64;
Query Match 57.2%; Score 1482; DB 1; Length 533;
Best Local Similarity 61.3%; Pred. No. 2.e-67;
Matches 284; Conservative 75; Mismatches 98; Indels 6; Gaps 3;
QY 4 KPNRRPSNTVLPYQTPRLRDYLLGKLGQGGQGTTLCTEKTSTANYACKSIPKRLV 63
DB 67 KPTP-----DTILGKYDDVRSVSYLGKELGRGQGVTVLCTEIASGKQYACKSISKEKLV 122
QY 64 CREYEDVWREIQIMHILSEHPNVRIKGTVEDSVFVHIVMEVCEGGELFDRIVSKGHS 123
DB 123 SKADKEDIRREIQIMHLSGQGNIVFEFGAYEDKSNVHVMVWELCAGGELFDRIAKGHS 182
QY 124 EBAVKLIITLIGWEACHSLGVMRDLPENFLFSDPKDAKLTDFGLSVFYKPGQY 183
DB 183 ERAATICRAVNVNICHFMGMVRDLKPENFLATKEENAMLTDFGLSVFIEGKM 242
QY 184 LYDVSGPYVAPEVLKCYGPEIDVWSAGVILYLLSGVPPFVAETSGIFPIILOGKL 243
DB 243 YRDIVGSYVAPEVLRNRYGKIDVWSAGVILYLLSGVPPFVAETSGIFDAILQGEI 302
QY 244 DFKSDPWPITSAKDLIYKMLERPKRISAEALCHPWTVDQAPDKPLDPAVLSRL 303
DB 303 DFEQWPSPISAKDLVRLMTQDPKRIITSAQVLQHPWLRDGEAS-DKPIDSAVLSRM 361
QY 304 KQPSQNKIKOMALRYIARLSEEEIGGLKELFKWIDTNSGTTTFEELKAGLRKVGSEL 363
DB 362 KQFRANKLKOMALKVIASNLNEEIKGLQKMTNMDTNSGTTTFEELKAGLRKAGLSKL 421
QY 364 MESEIKSLDCAADINDSGIDYGEFLAATLHNMKVEREILLVAEFDKDGSGVITIDE 423

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Db 422 SRAEVKQLWEADVNGSIDYVEFITATMERHKLERDEHLKFAQYFDKNSGFITRDE 481
QY 424 LOSACRGLCDT-PLDDMIKEIDLNDGKIDPSEFTAMRKG 465
DB 482 LESALIEHEMGDTSTIKDILSEVDFTDNDGRINYEFCAMRGG 524

RESULT 5
CDP2_MAIZE STANDARD; PRT; 513 AA.
ID CDP2_MAIZE
AC P49101;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Calcium-dependent protein kinase 2 (EC 2.7.1.1-) (CDPK 2).
GN CDPK2.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Merrit; TISSUE=Root tip;
RX MEDLINE=95281563; PubMed=7761420;
RA Patil S.; Takezawa D.; Poovalan B.W.;
RT "Chimeric plant calcium/calmodulin-dependent protein kinase gene with
RT a neural visinin-like calcium-binding domain.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:4897-4901(1995).
CC -1- FUNCTION: MAY PLAY A ROLE IN SIGNAL TRANSDUCTION PATHWAYS THAT
CC INVOLVE CALCIUM AS A SECOND MESSENGER.
CC -1- ENZYME REGULATION: ACTIVATED BY CALCIUM (BY SIMILARITY).
CC AUTOPHOSPHORYLATION MAY PLAY AN IMPORTANT ROLE IN THE REGULATION
CC OF THE KINASE ACTIVITY (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CAMK SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
CC -----
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CC -----
EMBL; U28376; AAA69507.1; -.
HSP; Q63450; IA06.
MaizeDB; 56895; -.
InterPro; IPR002048; EF-hand.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
Pfam; PF00036; ehand; 4.
Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Euk_pkinase; 1.
ProDom; PD000012; EF-hand; 2.
SMART; SM00054; EFh; 4.
SMART; SM00220; S_TKC; 1.
PROSITE; PS00018; EF HAND; 4.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
Transferrase; Serine/threonine-protein kinase; ATP-binding;
KW Calcium-binding; Phosphorylation.
KW DOMAIN 65 323
FT NP_BIND 71 79 ATP (BY SIMILARITY).
FT BINDING 94 94 ATP (BY SIMILARITY).
FT ACT_SITE 189 189 BY SIMILARITY.
FT CA_BIND 379 390 EF-HAND 1 (POTENTIAL).
FT CA_BIND 415 426 EF-HAND 2 (POTENTIAL).
FT CA_BIND 451 462 EF-HAND 3 (POTENTIAL).
FT CA_BIND 486 497 EF-HAND 4 (POTENTIAL).

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Query Match 55.2%; **Score** 1432.5; **DB 1;** **Length** 532;
Best Local Similarity 59.1%; **Pred.** No. 6.5e-67;
Matches 278; **Conservative** 76; **Mismatches** 107; **Indels** 9; **Gaps** 5
QY 2 ETXPN--PR---RP-SNTVLPQTFRLEPDHYLLGKLGQGFGTITCTSKTSANYACK 55

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DR SMART; SM00220; S TKC; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR TRANSFERASE; Serine/threonine-protein kinase; ATP-binding;
KW Repeat.
FT DOMAIN 20 40 3 X 7 AA TANDEM REPEATS OF S-[LI]-P-X-X-
D-X.
FT REPEAT 20 26 1.
FT REPEAT 27 33 2.
FT REPEAT 34 40 3.
FT DOMAIN 148 410.
FT NP_BIND 148 410.
FT BINDING 150 180.
FT ACT_SITE 276 276.
FT DOMAIN 465 476.
FT DOMAIN 502 513.
FT DOMAIN 542 553.
FT DOMAIN 574 585.
FT SEQUENCE 602 AA; 67184 MW; 1D10BF68B37BF447 CRC64;
Query Match 32.9%; Score 854; DB 1; Length 602;
Best Local Similarity 41.2%; Pred. No. 5.1e-36;
Matches 184; Conservative 90; Mismatches 155; Indels 18; Gaps 8;
QY 28 LGKLGQGFSTYLCSTKSTANY-----ACKSIPKRLVCRDVEDVWREIQIMHLS 82
DB 150 VGEVGHGFG--YTRAKPKKGFQGVAVKVPKAKNTAIEDVRRVKILRALT 207
QY 83 EHNVVRKIGTSDYSFVHIVMEVCGGELDFRIVSK-GHFSEREAVKLIKTLGVFAEC 141
DB 208 GHNVLQVDAFEDHTNYYVMELCEGGLDRLSRGKGKYTEDDAKAVMIQILNVAFV 267
QY 142 HSLGVMRDLKPNFLPDSKDKAKLKATDFGLSVKPKGVLYDVGSPYVAVPEVLKK 201
DB 268 HLQGVVRDLKPNFLPDSKDKAKLKATDFGLSVKPKGVLYDVGSPYVAVPEVLHR 327
QY 202 CYGPEIDWSAGVILYLLSGVPPFWAETESGIFRILQGLKDFKSDPWTISEAAKDLI 261
DB 328 SYSTEADVMSIGVISYLLGSRFPFWARTESGIFRAVLKANLSFDPPWFSVSEAKDFV 387
QY 262 YKMLERPKKRISHEALCPHWIVDEQAQPKLDPAVLSRLKQFSQMKIKMALRVIA 321
DB 388 KRLNKDKPRKMTAAQALCHSWIKNSNDI-KFFELDLVFLKMLKVMYRSPRKAAALRLS 446
QY 322 ERLSEEGIGLKELPKMIDTNSGTTTFEELKAGLRVGSSELM-ESEIKSLMDAADIINS 380
DB 447 KTLVDELFLYKEQFVLLEPTKNGTISLENIKQALNRNSTDAMKDSRVLDLVSLNALQY 506
QY 381 GTIDYGFLLAATLHNNKVER-----EELVAFSDFDKSGGYTTIDELQSACTEFLCPT 436
DB 507 RRMDFEFCAALSHVQLEALDRWEQCHARCAYDLFEKDGNRNIMIBELAS---ELGLGFS 563
QY 437 -PLDDMIKEIDLNDGKIDTSEPTAVM 462
DB 564 IPVAVLHDWIRHTDGLKSLFLGVYKLL 590
RESULT 9
ID_KCCD_HUMAN STANDARD; PRT; 499 AA.
AC Q13557; Q9UGF9; Q9UGH6;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calcium/calmodulin-dependent protein kinase type II delta chain (EC
DE 2.7.1.123) (Cam-kinase II delta chain) (Cam kinase II delta subunit)
DE (CAMK-II delta subunit).
GN CAMK2D.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
```

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CC EMBL; L24907; AAA19670.1; --
CC EMBL; L26288; AAA66944.1; --
CC PDB; 1A06; 08-APR-98.
CC InterPro; IPR000719; Euk_pkinase.
CC InterPro; IPR002290; Ser_thr_pkinase.
CC Pfam; PF00069; pkinase; 1.
CC ProDom; PDC00001; Euk_pkinase; 1.
CC SMART; SM00220; S_TKc; 1.
CC PROSITE; PS00107; PROTEIN KINASE ATP; 1.
CC PROSITE; PS00108; PROTEIN KINASE-ST; 1.
CC PROSITE; PS00111; PROTEIN KINASE-DOM; 1.
CC Transferrase; Serine/threonine-protein kinase; Calmodulin-binding;
KW Phosphorylation; ATP-binding; Alternative splicing; 3D-structure.
FT DOMAIN 20 276 PROTEIN KINASE.
FT NP BIND 26 34 ATP (BY SIMILARITY).
FT BINDING 49 49 ATP (BY SIMILARITY).
FT ACT SITE 141 141 BY SIMILARITY.
FT MOD RES 177 177 PHOSPHORYLATION (AUTO-).
FT VARSPLIC 323 374 TSQGGQTASHGELLTPTAGGAGCCGACCCDCCVPGSELP
FT PAPPFSSRAN -> HQPGGTGDS (IN 37 KDA ISOFORM).
FT CONFLICT 112 112 F -> G (IN REF. 1).
FT CONFLICT 118 118 A -> R (IN REF. 1).
FT CONFLICT 309 309 A -> R (IN REF. 1).
FT SEQUENCE 374 AA; 41638 MW; 37889B3DEF03AB2 CRC64;
Query Match 22.7%; Score 589.5; DB 1; Length 374;
Best Local Similarity 41.6%; Pred. No. 4.7e-23;
Matches 124; Conservative 56; Mismatches 113; Indels 5; Gaps 4;
Qy 18 QTPRLRHLLGKLGQGGFGTYLCTEKSTANVACKSIPKRLKVCREDYEDVWREIQI 77
Db 12 QAEIRDIDYFDVLTGAFSEVLAEDKRTQKLVAKIAKALEGREG--SMENEIIV 69
Qy 78 MHLSEHPNVRIKGTVEYDFVHIVMEVCEGGEFLDRIVSKGHFSEAEVLIKTLGV 137
Db 70 LHKI-KHPNIVALDDIVSGGHLVLIQLVSGGELFDRIKVEKGFYTERDASRLIFQVLD 128
Qy 138 VEACHSLGVNHRDLKPNFLPDSKDKAKATDFGLSVFYKFGQYLYDVVCSYVVAPE 197
Db 129 VKYLDHDLGIVHRDLKPNFLPDSKDKAKATDFGLSVFYKFGQYLYDVVCSYVVAPE 188
Qy 198 VL-KKCYGPEIDVMSAGVILYLLSGVPPFWAETESGIFRQILQGLDFKSDPWPITISEA 256
Db 189 VLAQKPYSKAVDCWSIGVIAVILLCGVPFYDENDAKLFEQILKAEYFDSYWDSDS 248
Qy 257 AKDIIYKMLERSPKRISAHEALCHPWIVDEQAAPKPLDPAVLSRLKQFSQWNKIKK 314
Db 249 AKDFIRHLMKDEPKRTCEQALQHPWIAGDTAL-DKNTHQSVSSQIKKQFAKSKWKQ 305
RESULT 11
KCCI_HUMAN STANDARD; PRT; 370 AA.
ID KCCI_HUMAN
AC Q14012;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Calcium/calmodulin-dependent protein kinase type I (EC 2.7.1.123)
DE (CAM kinase I).
GN CAMK1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Db 9 RFTDEYQLFEELGKGAFAFVVRRCMKIPTGQGAARIINTKKLSAF-DHOKLEREARC-R 66
Qy 81 LSHHPNVRIKGTVEYDFVHIVMEVCEGGEFLDRIVSKGHFSEAEVLIKTLGVVEA 140
Db 67 LLKHPNIVRLHDSISEGHHYLVDFDLTGELFEDIVAREYSEADASHCIQILSVNH 126
Qy 141 CHSLGVNHRDLKPNFLPDSKDKAKATDFGLSVFYKFGQYLYDVVCSYVVAPEVL 199
Db 127 CHLNGIVHRDLKPNFLPDSKDKAKATDFGLSVFYKFGQYLYDVVCSYVVAPEVL 186
Qy 200 KK-CYGEIDVMSAGVILYLLSGVPPFWAETESGIFRQILQGLDFKSDPWPITISEAAK 258
Db 187 RKPYPKVPDVAAGVILYLLSGVPPFWAETESGIFRQILQGLDFKSDPWPITISEAAK 246
Qy 259 DLIYKMLERSPKRISAHEALCHPWIVDEQAAPKPLDPAVLSRLKQFSQWNKIKMALR 318
Db 247 DLINKMLTINPAKRTASEALKHPICQRTSVASMHROETVDCLEKFNARRKLG--A 303
Qy 319 VIARLSSEIEIGGLKELFKMID-----TNSG-TITFELKA---GLKRVGSELMESEIK 369
Db 304 ILTMTLATRNFSAKSLKPKDGVKVESTSSNTTIDEDVQKARKQELIKVTQLIEA--- 360
Qy 370 SLMDAADIDNSGTIDYGEFLAAT 392
Db 361 -----INNGDFEAYT 370
RESULT 10
KCCI_RAT STANDARD; PRT; 374 AA.
ID KCCI_RAT
AC Q63450; Q63084;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Calcium/calmodulin-dependent protein kinase type I (EC 2.7.1.123)
DE (CAM kinase I).
GN CAMK1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
[1] SEQUENCE FROM N.A. (37 KDA ISOFORM).
MEDLINE=94075341; PubMed=8253780;
Picciotto M.R., Czernik A.J., Nairn A.C.;
"Calcium/calmodulin-dependent protein kinase I. cDNA cloning and identification of autophosphorylation site.";
J. Biol. Chem. 268:26512-26521(1993).
[2] SEQUENCE FROM N.A. (42 KDA ISOFORM).
STRAIN=Sprague-Dawley; TISSUE=lung;
MEDLINE=95035115; PubMed=7948038;
Cho F.S., Phillips K.S., Bogucki B., Weaver T.E.;
"Characterization of a rat cDNA clone encoding calcium/calmodulin-dependent protein kinase I.";
Biochim. Biophys. Acta 1224:156-160(1994).
[3] X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF SHORT FORM.
TISSUE=Brain;
MEDLINE=96182648; PubMed=8601311;
Goldberg J., Nairn A.C., Kuriyan J.;
"Structural basis for the autoinhibition of calcium/calmodulin-dependent protein kinase I.";
Cell 84:875-887(1996).
CC -!- FUNCTION: PHOSPHORYLATES SYNAPSIN I.
CC -!- CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.
CC -!- ENZYME REGULATION: ACTIVATED BY CA++/CALMODULIN. MUST BE PHOSPHORYLATED TO BE MAXIMALLY ACTIVE.
CC -!- SUBUNIT: MONOMER.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -!- CAMK SUBFAMILY.


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DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002230; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD00001; Euk_pkinase; 1.
DR SMART: SM00220; S_TK; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
DR Transferase: Serine/threonine-protein kinase; ATP-binding;
KW Calmodulin-binding.
KW DOMAIN 46 300 PROTEIN_KINASE.
FT NP_BIND 52 60 ATP (BY SIMILARITY).
FT BINDING 75 75 ATP (BY SIMILARITY).
FT ACT_SITE 164 164 BY SIMILARITY.
FT DOMAIN 322 341 CALMODULIN-BINDING (POTENTIAL).
SQ SEQUENCE 473 AA; 51925 MW; EFEE51E5612326DC CRC64;

Query Match 22.3%; Score 578.5; DB 1; Length 473;
Best Local Similarity 37.2%; Pred. No. 2.1e-22;
Matches 140; Conservative 65; Mismatches 144; Indels 27; Gaps 10;

QY 22 LRDRHYLLGKLGQGGFGTTVLTCTEKTSTANYACKSIPKRLKVCREDYEDVVRQIMHHL 81
DB 42 LSDPFEVESLGRGATSVYRCQKGTQKPYALKVLK-----TVDKKIVRTGIVLLRL 96
QY 82 SEHPNVVRKGTVEDSVFVHVMVEVCEGGELFDRIKSVKGFHSREAVKLIKILGWVEAC 141
DB 97 S-HPNIIKLEIFETPTETISLVLELVLTGGELFDRIKSVKGFHSREAVKLIKILGWVEAC 155
QY 142 HSLGVMHRLDKPENFLDSPKDDAKLKATDFGLSVFKPGQVLYDVVGSPYVVAPEVLAK 201
DB 156 HENGIVHRDLKPELNLATAPDAPLKIADFGLSKIVEHQVLMTKTCGTFGYCAPEILRG 215
QY 202 C-YGPEIDVWSAGVILYLSGVPPFWAET-ESGIFQILQGLKDFKSPDPWPTISBAKD 259
DB 216 CAYGPEIDVWSAGVILYLSGVPPFWAET-ESGIFQILQGLKDFKSPDPWPTISBAKD 275
QY 260 LIYKMLERSPKRISAEALCHPMIVDSQAPDKPLDPAVLSLKQFSQWKIKKMLRV 319
DB 276 LVRLKLVLDPKRRLTTFQALQHPWTG-KAANFVHMDTA-QKQLQGFNARKLKAIVKAV 333
QY 320 IA-ERL--SEIEIGLKELFKW-----IPTDNGSTITFEE-----LKAGLKVGVSE 362
DB 334 VASSRLGSSASSHSGSIQBSKASRDPSPIDQGNEDMKAIPEGEKIQDGAQAQAVKGAQAE 393
QY 363 LMSEIKSLMDAADI 378
DB 394 LMKVQALEKVKGADIN 409

RESULT 13
KCDD RAT
ID KCDD RAT STANDARD; PRT; 533 AA.
AC F15791;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calcium/calmodulin-dependent protein kinase type II delta chain (EC
DE 2.7.1.123) (CaM-kinase II delta chain) (CaM kinase II delta subunit)
DE (CaMK-II delta subunit).
GN CAWK2D.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]_
RP SEQUENCE FROM N.A.
RX MEDLINE=90036861; PubMed=2553697;
RA Tobimatsu T., Fujisawa H.;
RT "Tissue-specific expression of four types of rat calmodulin-dependent
RT protein kinase II mRNAs."
RL J. Biol. Chem. 264:17907-17912 (1989).
DB [2]

```

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RP SEQUENCE OF 314-533 FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Aorta, and Skeletal muscle;
RX MEDLINE=93300844; PubMed=8390994;
RA Schworer C.M., Rothblum L.I., Thekkumkara T.J., Singer H.A.;
RT "Identification of novel isoforms of the delta subunit of
RT Ca2+/calmodulin-dependent protein kinase II. Differential expression
RT in rat brain and aorta."
RL J. Biol. Chem. 268:14443-14449 (1993).
CC -!- FUNCTION: THIS KINASE MAY PLAY A ROLE IN NEUROTRANSMISSION.
CC -!- CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.
CC -!- ENZYME REGULATION: AUTOPHOSPHORYLATION OF CAM-KINASE II PLAYS AN
CC -!- IMPORTANT ROLE IN THE REGULATION OF THE KINASE ACTIVITY.
CC -!- SUBUNIT: COMPOSED OF FOUR DIFFERENT CHAINS: ALPHA, BETA, GAMMA,
CC -!- AND DELTA.
CC -!- ALTERNATIVE PRODUCTS: 4 ISOFORMS; DELTA 1 (SHOWN HERE), DELTA 2,
CC -!- DELTA 3 AND DELTA 4; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- TISSUE SPECIFICITY: DELTA 1 IS THE PREDOMINANT FORM IN THE
CC -!- BRAIN, DELTA 2 AND 3 PREDOMINATE IN THE AORTA AND DELTA 4
CC -!- IN SKELETAL MUSCLE.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -!- CAWK SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: J05072; AAA40866.1; -
DR EMBL: L13406; AAA41479.1; -
DR EMBL: L13407; AAA41480.1; -
DR EMBL: L13408; AAA41481.1; -
DR PIR: A34366; A34366.
DR HSP: Q83450; LA06.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002230; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD00001; Euk_pkinase; 1.
DR SMART: SM00220; S_TK; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
DR Transferase: Serine/threonine-protein kinase; Calmodulin-binding;
KW Phosphorylation; ATP-binding; Neurone; Alternative splicing.
KW DOMAIN 14 272 PROTEIN_KINASE.
FT NP_BIND 20 28 ATP (BY SIMILARITY).
FT BINDING 43 43 ATP (BY SIMILARITY).
FT ACT_SITE 136 136 BY SIMILARITY.
FT DOMAIN 291 301 CALMODULIN-BINDING (BY SIMILARITY).
FT VARSPPLIC 329 362 MISSING (IN ISOFORM DELTA 2).
FT VARSPPLIC 329 335 INKANV -> KRKSSV (IN ISOFORM DELTA 3).
FT VARSPPLIC 337 359 MISSING (IN ISOFORM DELTA 3).
FT VARSPPLIC 360 362 GNK -> QMM (IN ISOFORM DELTA 3).
FT VARSPPLIC 349 362 MISSING (IN ISOFORM DELTA 4).
SQ SEQUENCE 533 AA; 60080 MW; E413CB2B5A0E7CA CRC64;

Query Match 22.2%; Score 574.5; DB 1; Length 533;
Best Local Similarity 39.4%; Pred. No. 3.8e-22;
Matches 127; Conservative 54; Mismatches 134; Indels 7; Gaps 5;

QY 21 LRDRHYLLGKLGQGGFGTTVLTCTEKTSTANYACKSIPKRLKVCREDYEDVVRQIMHHL 80
DB 9 RFTDEYQFELGKGAFSVVRCNKIPTGQYAAKINTKLSAR-DHOKLEAREAFIC-R 66
QY 81 LSEHPNVVRKGTVEDSVFVHVMVEVCEGGELFDRIKSVKGFHSREAVKLIKILGWVEA 140
DB 67 LLKHPNIVRLHDSISREGPHYLPDLVTGGELFEDIVAREYVSEADASHCIQOILESVMH 126
QY 141 CHSLGVHRLDKPENFLDSPKDDAKLKATDFGLSVFKPGQVLYDVVGSPYVVAPEVL 199
DB 127 CHLNGIVHRDLKPELNLATAPDAPLKIADFGLSKIVEHQVLMTKTCGTFGYCAPEILRG 186

```

QY 200 KK-CYGPEDVWSAGVILYLLSGVPPWPAETESGIFRQILQKLDKSPWPTTGEAAK 258
 DB 187 RNDPKYKPVDMWACGVILYLLSGVPPWDDQRLVQQIKAGAYDFPSEWTVTPEAK 246
 QY 259 DLIYKXKLSRPPKRISAHEALCHPWVDEQAAPDKPLDPAVLISLKQFSQWNIKKWALR 318
 DB 247 DLINKVLTINPAKRITASEALGHPWCQSTVASMHRQETVDCIKFNARRKLKG---A 303
 QY 319 VIAERLSEEEIGGLKELFQWID 340
 DB 304 ILTMTLATRNFAAKSLKXPD 325

RESULT 14
 KCC4 MOUSE STANDARD; PRT; 469 AA.
 AC P08414; Q61381;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Calcium/calmodulin-dependent protein kinase type IV catalytic chain
 DE (EC 2.7.1.123) (CAM kinase-GR) (CaMK IV).
 GN CAMK4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Brain;
 RX JONES D.A., Glod J., Wilson-Shaw D., Hahn W.E., Sikela J.M.;
 RA Medline=91372388; PubMed=1933997;
 RT "cDNA sequence and differential expression of the mouse
 RT Ca2+/calmodulin-dependent protein kinase IV gene."
 RL FEBS Lett. 289:105-109(1991).
 RN [2]
 RP SEQUENCE OF 240-469 FROM N.A.
 RX MEDLINE=89122027; PubMed=2536634;
 RA Sikela J.M., Law M.L., Rao F.-T., Hartz J.A., Wei Q., Hahn W.E.;
 RT "Chromosomal localization of the human gene for brain
 RT Ca2+/calmodulin-dependent protein kinase type IV."
 RL Genomics 4:21-27(1989).
 RN [3]
 RP SEQUENCE OF 315-469 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=87204263; PubMed=3033675;
 RA Sikela J.M., Hahn W.E.;
 RT "Screening an expression library with a ligand probe: isolation and
 RT sequence of a cDNA corresponding to a brain calmodulin-binding
 RT protein."
 RL Proc. Natl. Acad. Sci. U.S.A. 84:3038-3042(1987).
 CC -1- CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.
 CC -1- SUBCELLULAR LOCATION: SUBSTANTIAL LOCALIZATION IN CERTAIN NEURONAL
 CC NUCLEI.
 CC -1- TISSUE SPECIFICITY: BRAIN AND TESTIS.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC CAMK SUBFAMILY.

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 EMBL; M16206; AAA39933.1; --
 EMBL; M64266; AAA37364.1; --
 EMBL; J03057; AAA37366.1; --
 EMBL; X58995; CAA41741.1; --
 PIR; A29878; A29878.
 PIR; S17656; S17656.

DR HSP; Q63450; 1A06.
 DR MGD; MGI:88258; Camk4.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR Pfam; PF00049; pkinase; 1.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR SMART; SMO0202; S_TKC; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
 KW Transferase; Serine/threonine-protein kinase; ATP-binding;
 KW Calmodulin-binding.
 FT DOMAIN 42 296 PROTEIN KINASE.
 FT NP_BIND 48 56 ATP (BY SIMILARITY).
 FT BINDING 71 71 ATP (BY SIMILARITY).
 FT ACT_SITE 160 160 BY SIMILARITY.
 FT DOMAIN 318 337 CALMODULIN-BINDING (POTENTIAL).
 FT CONFLICT 278 280 VLD -> CFGI (IN REF. 2).
 FT CONFLICT 302 302 N -> T (IN REF. 2).
 SQ SEQUENCE 469 AA; 52627 MW; CE1F98670822F975 CRC64;
 Query Match 22.1%; Score 574; DB 1; Length 469;
 Best Local Similarity 33.4%; Pred. No. 3.6e-22;
 Matches 146; Conservative 79; Mismatches 170; Indels 42; Gaps 12;

QY 22 LRHYLLGKLGQGFQGTLYLCTEKSTSANVACKSIKPKLVCRDVEDYVMEIQLMHL 81
 DB 38 LGDFEVESELGRGATSIYRCKQKQKQKPYALAVLK---TVDKKIVRTIGVLLRL 92
 QY 82 SEHPNVIRKGTYESVVFHIVMEVCEGGELFDRIKSGHFSEREAVKLITLGVVEAC 141
 DB 93 S-HPNIIKIKETFTPTTEISLVLELVGTGELFDRIKSGYSEKRDARDVAKQILEAVYL 151
 QY 142 HSLGVHRLDKPENLFDSPKDDAKLKATDFGLSVFVKPGQYLYDVVGSFYVVAPEVLKK 201
 DB 152 HENGIVHRLDKPENLLYATPADPLKATDFGLSKIYEHQVLMKTVCGTFCYCAPEILRG 211
 QY 202 C-YGPEIDVMSAGVILYLLSGVPPWPAET-ESGIFRQILQKLDKSPWPTTSEAKD 259
 DB 212 CAYGPEVDVMSVGIITILLGCFEPFYDERGQCFMFRILNCEYFFISPMWDEVSLNAKD 271
 QY 260 LIYKMLERSPKRISAEALCHPWVDEQAAPDKPLDPAVLISLKQFSQWNIKKWALRV 319
 DB 272 LVKRLVLDPKRRLTTFQALQHPWVIG-KAANFVHMDTA-OKKLOEFNARKKLAAKAV 329
 QY 320 IABRLSEEBIGGLKELFKMIDTD---NSGTITFEELKAGLRVGSSELMESEIKSLMDAAD 376
 DB 330 VA---SSRLGSASSHTSIQENHKASSDPPSTQAKDSTLLGKKMQEEDQE- 379
 QY 377 IDNSGTIDYGEFLAATLHNKMKEREILVAASFQDKDGSVITIDELQSACTFEGLCDT 436
 DB 380 -----DQVEAERSADEMRKQSEEV-----EKDAG--VKEETSSMVPQDPEDL 422
 QY 437 PLDDMIKEIDLNDGKI 453
 DB 423 ETDD--PEMKRSEKKL 437

RESULT 15
 KCC4 RAT STANDARD; PRT; 474 AA.
 AC P13234;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Calcium/calmodulin-dependent protein kinase type IV catalytic chain
 DE (EC 2.7.1.123) (CAM kinase-GR) (CaMK IV) (Calipermin).
 GN CAMK4.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=101116;
 RN [1]

SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND PARTIAL SEQUENCE.
 RP MEDLINE=91289548; PubMed=1648230;
 RA Ohmsted C.-A., Bland M.M., Werrill B.M., Sahyoun N.;
 RT "Relationship of genes encoding Ca2+/calmodulin-dependent protein
 RT kinase Gr and calpermin: a gene within a gene.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:5784-5788(1991).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RX MEDLINE=91304387; PubMed=1649385;
 RA Means A.R., Cruzalegui F., Lemagueresse B., Needleman D.S.,
 RA Slaughter G.R., Ono T.;
 RT "A novel Ca2+/calmodulin-dependent protein kinase and a male germ
 RT cell-specific calmodulin-binding protein are derived from the same
 RT gene.";
 RL Mol. Cell. Biol. 11:3960-3971(1991).
 RN [3]
 RP SEQUENCE OF 250-474 FROM N.A. (ISOFORM 1).
 RX STRAIN=Sprague-Dawley; TISSUE=Brain;
 RX MEDLINE=89174647; PubMed=2538431;
 RA Ohmsted C.-A., Jensen K.F., Sahyoun N.;
 RT "Ca2+/calmodulin-dependent protein kinase enriched in cerebellar
 RT granule cells. Identification of a novel neuronal
 RT calmodulin-dependent protein kinase.";
 RL J. Biol. Chem. 264:5866-5875(1989).
 RN [4]
 RP SEQUENCE OF 306-474 FROM N.A. (ISOFORM 2), AND SEQUENCE OF 335-361.
 RX STRAIN=Sprague-Dawley;
 RX MEDLINE=89123272; PubMed=2914893;
 RA Ono T., Slaughter G.R., Cook R.G., Means A.R.;
 RT "Molecular cloning sequence and distribution of rat calpermin, a
 RT high affinity calmodulin-binding protein.";
 RL J. Biol. Chem. 264:2081-2087(1989).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RX MEDLINE=96094352; PubMed=7493991;
 RA Sun Z., Means R.L., Lemagueresse B., Means A.R.;
 RT "Organization and analysis of the complete rat calmodulin-dependent
 RT protein kinase IV gene.";
 RL J. Biol. Chem. 270:23507-23514(1995).
 CC -1- FUNCTION: CAM KINASE GR IS A NEURONAL-SPECIFIC PROTEIN KINASE,
 CC ENRICHED IN CEREBELLAR GRANULE CELLS.
 CC -1- FUNCTION: CALPERMIN IS A HEAT-STABLE, ACIDIC, CALMODULIN-BINDING
 CC PROTEIN.
 CC -1- CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms: 1/calcium-calmodulin-dependent
 CC protein kinase type IV catalytic chain (shown here) and
 CC 2/calpermin; are produced by alternative splicing.
 CC -1- TISSUE SPECIFICITY: Isoform 1 is expressed in brain and isoform 2
 CC is testis-specific.
 CC -1- PTM: THE N-TERMINAL OF CALPERMIN IS BLOCKED.
 CC -1- MISCELLANEOUS: The presence of an alternative promoter gives rise
 CC to the testis-specific isoform 2/calpermin protein.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC CAMK SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL; M63334; AAA40865.1; -;
 DR EMBL; M74488; AAA40845.1; ALT_SEQ.
 DR EMBL; M64757; AAA40856.1; -;
 DR EMBL; M64757; AAA40857.1; -;
 DR EMBL; J04600; AAA41867.1; -;
 DR EMBL; J04446; AAA40990.1; -;
 DR PIR; A41103; TVRTC4.
 DR HSP; Q63450; 1A06.
 DR InterPro; IPR000729; Euk_pkinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.

PFam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Euk_Dkinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00108; PROTEIN KINASE-ST; 1.
 DR PROSITE; PS00111; PROTEIN KINASE-DOM; 1.
 KW Transferase; Serine/threonine-protein kinase; ATP-binding;
 KW calmodulin-binding; Testis; Alternative splicing.
 FT DOMAIN 42 296
 FT NP BIND 48 56
 FT BINDING 71 71
 FT ACT SITE 160 160
 FT DOMAIN 318 337
 FT DOMAIN 333 399
 FT DOMAIN 403 413
 FT VARSPPLIC 1 305
 FT CONFLICT 372 372
 FT CONFLICT I -> M (IN REF. 2 AND 4).
 SQ SEQUENCE 474 AA; 53133 MW; 56F71AC5644DED23 CRC64;
 Query Match 22.1%; Score 572; DB 1; Length 474;
 Best Local Similarity 34.1%; Pred. No. 4.5e-22;
 Matches 142; Conservative 75; Mismatches 158; Indels 42; Gaps 11;
 QY 3 TRKN-PRRSNTVLPYQPRLRADHYLVKK-----LGQGPQTTLCTEKST 48
 DB 5 TVPSCPSPCSSVTSTENLVDPYWDGSKRDLPSDFEVESELGRGATSIYRCKQGT 64
 QY 49 SANYACKSIPIKRLVCREDEYEDVWREIOIMEHLSEHPNVRIKGTIEDSVFHVMEVCE 108
 DB 65 QKPYALKVLK-----TVDKKIVRTTEIGVLLRLS-HPNIIKLKEIFETPTTEISLVLELT 118
 QY 109 GGELFRIIVSKGHFSEREAVKILITLGVVEACHSLGVMDHDLKPNFLFDSPKDDAKLK 168
 DB 119 GGELFRIIVEKGYISERDAADAVKQILEAVAYLHENGIVHRLKPNLLYATPAPDAPLK 178
 QY 169 ATDFGLSVFKPGQVLYDVVGSPPYVAPEVLKVC-YGPEIDVMSAGVILYLILSGVPPFW 227
 DB 179 IADFGLSKIVEHQVLMKTVCGTPGYCAPILLRGCAYGFEVDMVSGIITVILLCGPPEFY 238
 QY 228 AET-ESGIFRQILQGLKDFKSDPWTISEAAKDLIYKMLERSPKKRISAHEALCHPWIVD 286
 DB 239 DERGDQFMFERILNCYYFISPMWDEVSINAKDLVKKLIVLDPKKRLTTTCAQHPPWTG 298
 QY 287 EQAAPKPLDPAVLRLKQFSQMKIKKMLRVIAERLSEEEIIGLKELFKMIDTNSGT 346
 DB 299 -KAANFVHMDTA-QKKLQEFNARRKKAQVAVVA-----SSRLGSASSSHNTIQESNKAS 352
 QY 347 ITFEELKAGLKRVGSELMESEIKSLMDAADIDNSGTDYGEFLAATLHMKNKEREHI 403
 DB 353 SRAQPAQDGKDK--TDPLENKIOA-----GDHEAAKAAADETKKLOSEEV 395

Search completed: February 13, 2003, 21:12:06
 Job time : 21 secs

GenCore version 5.1.3
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XM protein - protein search, using sw model

Run on: February 13, 2003, 20:59:17 ; Search time 74 seconds
(without alignments)
1378.288 Million cell updates/sec

Title: US-09-848-806-1
Perfect score: 2593
Sequence: 1 METKPNRPSTNVLPLYQTP.....KNLNFNIAAFGVDEKSD 495

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL 21:
1: sp_archea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_proteus.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_bacterioph.*
17: sp_archeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2593	100.0	495	10	Q39016 arabidopsis
2	2577	99.4	495	10	Q949P0 arabidopsis
3	2536	97.8	557	10	Q9LQH7 arabidopsis
4	2458	94.8	501	10	Q38869 arabidopsis
5	2030	78.3	490	10	Q24430 glycine max
6	1969.5	76.0	496	10	Q93X19 solanum tub
7	1844.5	71.1	490	10	Q42396 arabidopsis
8	1773	68.4	551	10	Q9FXQ3 oryza sativ
9	1752	67.6	452	10	Q04417 zea mays (m
10	1751	67.5	487	10	Q43676 phaseolus a
11	1745	67.3	554	10	Q04123 zea mays (m
12	1742	67.2	556	10	Q38871 arabidopsis
13	1739.5	67.1	578	10	Q93XJ0 solanum tub
14	1733.5	66.9	578	10	Q93YF3 nicotiana t
15	1731	66.8	544	10	Q38872 arabidopsis
16	1728	66.6	551	10	Q93YF4 nicotiana t

17	1719	66.3	646	10	Q38870
18	1717.5	66.2	578	10	Q24460
19	1709.5	65.9	573	10	Q38838
20	1709	65.9	483	10	Q39014
21	1708	65.9	581	10	Q93YF7
22	1700.5	65.6	484	10	Q9SZM3
23	1672.5	64.5	639	10	Q82107
24	1672.5	64.5	639	10	Q82107
25	1630	63.3	593	10	Q9ZV15
26	1592	61.4	451	10	Q41783
27	1587	61.2	542	10	Q9SNK9
28	1531.5	59.1	548	10	Q85003
29	1524.5	58.8	548	10	Q85724
30	1509.5	58.2	528	10	Q8VYE7
31	1506.5	58.1	528	10	Q8VYE7
32	1484.5	57.3	540	10	Q81390
33	1482	57.2	531	10	Q849U0
34	1482	57.2	531	10	Q849U0
35	1480	57.1	518	10	Q9AXA7
36	1480	57.1	531	10	Q41790
37	1475	56.9	347	10	Q94IQ5
38	1473	56.8	553	10	Q8RW36
39	1471.5	56.7	521	10	Q94KH6
40	1469.5	56.7	542	10	Q9AR92
41	1464.5	56.5	514	10	Q9AR15
42	1463.5	56.4	521	10	Q9C6P3
43	1462	56.4	529	10	Q42479
44	1462	56.4	534	10	Q9FRK2
45	1458.5	56.2	538	10	Q24431

ALIGNMENTS

RESULT 1
Q39016 PRELIMINARY; PRT; 495 AA.
ID Q39016
AC Q39016; (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Calcium-dependent protein kinase.
OS Arabidopsis thaliana (Mouse-ear cress).
GN Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLOMBIA;
RX MEDLINE=94359455; PubMed=8078458;
RA Hayashida N., Shinozaki K.,
RA Urao T., Katagiri T., Mizoguchi T., Yamaguchi-Shinozaki K.,
RT "Two genes that encode Ca2+-dependent protein kinases are induced by
RT drought and high-salt stresses in Arabidopsis thaliana.";
Mol. Gen. Genet. 244:331-340(1994)
RL -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

EMBL; D21806; BAAC4830.1; --
DR HSSP; P02593; 1FW4.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00036; ehand; 4.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 1.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFL; 4.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00108; EF HAND; UNKNOWN 4.
DR PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS0108; PROTEIN_KINASE_ST; 1.

KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferrase.
SQ SEQUENCE 495 AA; 5867 MW; 5909A451242C3A6D CRC64;

Query Match 100.0%; Score 2593; DB 10; Length 495;
Best Local Similarity 100.0%; Pred. No. 9.5e-183;
Matches 495; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 METKNPRPNTVLPYOTPLRDHYLLGKLGOGGTLYLCTEKSTANYACKSIPKR 60
DB 1 METKNPRPNTVLPYOTPLRDHYLLGKLGOGGTLYLCTEKSTANYACKSIPKR 60

QY 61 KLVCRDVEDVWREIQMHLSHPNVVRIGTYEDSVFVHIWMEVCEGGEFDRIVSKG 120
DB 61 KLVCRDVEDVWREIQMHLSHPNVVRIGTYEDSVFVHIWMEVCEGGEFDRIVSKG 120

QY 121 HFSEREAVKLITLGVVEACHSLGVWHRDLKPNFLFDSPKDDAKLKATDFGLSVFYKP 180
DB 121 HFSEREAVKLITLGVVEACHSLGVWHRDLKPNFLFDSPKDDAKLKATDFGLSVFYKP 180

QY 181 GOYLYDVVGSPPYVAPEVLKCYGPEIDVMSAGVILYLLSGVPPFWAETESGIFRQILQ 240
DB 181 GOYLYDVVGSPPYVAPEVLKCYGPEIDVMSAGVILYLLSGVPPFWAETESGIFRQILQ 240

QY 241 GKLDPKSPWPPTISEAAKDLIYKMLSPKRI SAHALCHPWIVDEQAAPDKPLDPAVL 300
DB 241 GKLDPKSPWPPTISEAAKDLIYKMLSPKRI SAHALCHPWIVDEQAAPDKPLDPAVL 300

QY 301 SRLKQFSQWNIKKQALRVIAERLSEIEIGLKFPMIDTNSGTTITFEELKAGLKRVG 360
DB 301 SRLKQFSQWNIKKQALRVIAERLSEIEIGLKFPMIDTNSGTTITFEELKAGLKRVG 360

QY 361 SELMESEIKSLMDAADI NSGTIDYGFLLAATLHMKNVREIEILVAAFDFDKGSGYIT 420
DB 361 SELMESEIKSLMDAADI NSGTIDYGFLLAATLHMKNVREIEILVAAFDFDKGSGYIT 420

QY 421 IDELOSACTEFGCLDTPDDMIKIDLDNKGIDFSEFTAMRKGDGVCGRSRTMMKNLNF 480
DB 421 IDELOSACTEFGCLDTPDDMIKIDLDNKGIDFSEFTAMRKGDGVCGRSRTMMKNLNF 480

QY 481 NIADAFGVGDGKSDD 495
DB 481 NIADAFGVGDGKSDD 495

RESULT 2
Q949P0 PRELIMINARY; PRT; 495 AA.

AC Q949P0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Putative calcium-dependent protein kinase SK5.
GN F1504.8.

OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]_TaxID=3702;
RP SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Pham P.K., Banh J., Banno F., Dale J.M.,
RA Goldsmith A.D., Jiang P.X., Lee J.M., Onodera C.S., Quach H.B.,
RA Tang C., Toriumi M., Yamamura Y., Yu G., Yu S., Bowser L.,
RA Carling P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Kossema E., Lam B.,
RA Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
RA Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tracy S.R.,
RA Shiozaki K., Davis R.W., Ecker J.R., Theologis A.;
RT "Full length cDNA of gene F1504.8 (GI:878378).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY050981; AAK93658.1; -
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000719; Euk_pkinase.

DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00036; ehand; 4;
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 1.
DR ProDom; PD000012; EF-hand; 2.
DR ProSITE; PS00018; EF_HAND; UNKNOWN 4.
DR ProSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN 1.
DR ProSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR ProSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN 1.
KW ATP-binding; Kinase; Transferrase.
SQ SEQUENCE 495 AA; 55916 MW; 2DD0ED8C234EF2F7 CRC64;

Query Match 99.4%; Score 2577; DB 10; Length 495;
Best Local Similarity 99.6%; Pred. No. 1.4e-181;
Matches 493; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 METKNPRPNTVLPYOTPLRDHYLLGKLGOGGTLYLCTEKSTANYACKSIPKR 60
DB 1 METKNPRPNTVLPYOTPLRDHYLLGKLGOGGTLYLCTEKSTANYACKSIPKR 60

QY 61 KLVCRDVEDVWREIQMHLSHPNVVRIGTYEDSVFVHIWMEVCEGGEFDRIVSKG 120
DB 61 KLVCRDVEDVWREIQMHLSHPNVVRIGTYEDSVFVHIWMEVCEGGEFDRIVSKG 120

QY 121 HFSEREAVKLITLGVVEACHSLGVWHRDLKPNFLFDSPKDDAKLKATDFGLSVFYKP 180
DB 121 HFSEREAVKLITLGVVEACHSLGVWHRDLKPNFLFDSPKDDAKLKATDFGLSVFYKP 180

QY 181 GOYLYDVVGSPPYVAPEVLKCYGPEIDVMSAGVILYLLSGVPPFWAETESGIFRQILQ 240
DB 181 GOYLYDVVGSPPYVAPEVLKCYGPEIDVMSAGVILYLLSGVPPFWAETESGIFRQILQ 240

QY 241 GKLDPKSPWPPTISEAAKDLIYKMLSPKRI SAHALCHPWIVDEQAAPDKPLDPAVL 300
DB 241 GKLDPKSPWPPTISEAAKDLIYKMLSPKRI SAHALCHPWIVDEQAAPDKPLDPAVL 300

QY 301 SRLKQFSQWNIKKQALRVIAERLSEIEIGLKFPMIDTNSGTTITFEELKAGLKRVG 360
DB 301 SRLKQFSQWNIKKQALRVIAERLSEIEIGLKFPMIDTNSGTTITFEELKAGLKRVG 360

QY 361 SELMESEIKSLMDAADI NSGTIDYGFLLAATLHMKNVREIEILVAAFDFDKGSGYIT 420
DB 361 SELMESEIKSLMDAADI NSGTIDYGFLLAATLHMKNVREIEILVAAFDFDKGSGYIT 420

QY 421 IDELOSACTEFGCLDTPDDMIKIDLDNKGIDFSEFTAMRKGDGVCGRSRTMMKNLNF 480
DB 421 IDELOSACTEFGCLDTPDDMIKIDLDNKGIDFSEFTAMRKGDGVCGRSRTMMKNLNF 480

QY 481 NIADAFGVGDGKSDD 495
DB 481 NIADAFGVGDGKSDD 495

RESULT 3
Q91QH7 PRELIMINARY; PRT; 557 AA.

AC Q91QH7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE F1504.8.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]_TaxID=3702;
RP SEQUENCE FROM N.A.
RA Ecker J.R.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY050981; AAK93658.1; -
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000719; Euk_pkinase.

Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.

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RL 3]
RN
RP SEQUENCE FROM N.A.
RA Cheuk R., Shinn P., Brooks S., Buehler E., Chao O., Johnson-Hopson C.,
RA Khan S., Kim C., Alafai H., Bai B., Chin C., Chieu J., Choi E., Lam B.,
RA Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,
RA Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharly N.,
RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
RA Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
RA Theologis A., Ecker J.,
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AC007887; AAF79386.1; -.
DR HSP; P02593; 1FW4.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00036; ehand; 4.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 1.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 4.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS00018; EF HAND; UNKNOWN 4.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 557 AA; 63397 MW; 7E92BA5A6B3A240B CRC64;

Query Match 97.8%; Score 2536; DB 10; Length 557;
Best Local Similarity 88.5%; Pred. No. 1.8e-178;
Matches 493; Conservative 2; Indels 62; Gaps 1;

QY 1 METKPNRPSNTVLPYQTPRLRDHYLLKGLGQGFQGTLYLCTEKSTSANYSACKSIPIKR 60
DB 1 METKPNRPSNTVLPYQTPRLRDHYLLKGLGQGFQGTLYLCTEKSTSANYSACKSIPIKR 60

QY 61 KLVREDYEDVWEIQTIMHLSHPNVRKGTYESVVFHIVMEVCEGGELFDRIVSKG 120
DB 61 KLVREDYEDVWEIQTIMHLSHPNVRKGTYESVVFHIVMEVCEGGELFDRIVSKG 120

QY 121 HFSEREAVKLIKTILGVVEACHSLGVNHRDLKPEFLDSPKDDAKLKATDFGLSVFYK 180
DB 121 HFSEREAVKLIKTILGVVEACHSLGVNHRDLKPEFLDSPKDDAKLKATDFGLSVFYK 180

QY 181 ----- 180
DB 181 GLFLPWLIDSLILQVFLVFLVFSMNRKLKQSGFLJETGLLGFIMIANENKVFQMYRFD 240

QY 181 --GOYLVDVVGSPYYVAPELVKCYGPEIDVWAGVILYLLSGVPPFWAETESGIFRQI 238
DB 241 LFGQYLDVVGSPYYVAPELVKCYGPEIDVWAGVILYLLSGVPPFWAETESGIFRQI 300

QY 239 LQGLKDFKSPWPTISAAKDLIYKMLERSPKRISAHALCHPWVDSQAAAPDKPLDPA 298
DB 301 LQGLKDFKSPWPTISAAKDLIYKMLERSPKRISAHALCHPWVDSQAAAPDKPLDPA 360

QY 299 VLSRLKQFSQNKIKKVALRVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLKR 358
DB 361 VLSRLKQFSQNKIKKVALRVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLKR 420

QY 359 VGSLELMESEIKSLMDADIDNSGTIDYGEFLAATLHNKMEREEILVAAPSDFKDGSQY 418
DB 421 VGSLELMESEIKSLMDADIDNSGTIDYGEFLAATLHNKMEREEILVAAPSDFKDGSQY 480

QY 419 ITIDELQSACTEFGLCPTPLDDMKETDLDNDGKIDPFSEPTAMNRKGDGVGRSRTMMK 478
DB 481 ITIDELQSACTEFGLCPTPLDDMKETDLDNDGKIDPFSEPTAMNRKGDGVGRSRTMMK 540

QY 479 NFNIADAFGVGDGKSD 495
DB 541 NFNIADAFGVGDGKSD 557

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RESULT 4

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Q38869 PRELIMINARY; PRT; 501 AA.
ID Q38869;
AC Q38869;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Calmodulin-domain protein kinase CDPK isoform 4 (Fragment).
GN CPK4 OR T25P22.10 OR AT4G09570.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
[1]
SEQUENCE FROM N.A.
RC STRAIN=CV, COLUMBIA;
RA McCombie W.R.;
RT "Arabidopsis thaliana Genomic Sequence, Chromosome IV.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
[2]
SEQUENCE FROM N.A.
RN RA McCombie R.W., Spiegel L.A., Huang E.N., Nascimento L.U.,
RA de la Bastide M., Vil D.M., Preston R.R., Matero A., Shah R.,
RA O'Shaughnessy A., Rodriguez M., Shekher M., Schutz K., See L.H.,
RA Swaby I., Habermann K., Dedhia N.N., Mewes H.W., Lemcke K.,
RA Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[3]
SEQUENCE FROM N.A.
RN RA Spiegel L.A., Huang E.N., Nascimento L.U., de la Bastide M., Vil D.M.,
RA Preston R.R., Matero A., Shah R., O'Shaughnessy A., Rodriguez M.,
RA Shekher M., Schutz K., See L.H., Swaby I., Habermann K., Dedhia N.N.,
RA Mewes H.W., Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; U31752; AAB03243.1; -.
DR EMBL; AL161831; CAB82124.1; -.
DR EMBL; AL161515; CAB78080.1; -.
DR HSP; P02593; 1FW4.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00036; ehand; 4.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Euk_pkinase; 1.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 4.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS00018; EF HAND; UNKNOWN 4.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Kinase; Serine/threonine-protein kinase.
FT NON_TER 1
SQ SEQUENCE 501 AA; 56416 MW; C709C17DFAF74B70 CRC64;

Query Match 94.8%; Score 2458; DB 10; Length 501;
Best Local Similarity 94.8%; Pred. No. 8.6e-173;
Matches 470; Conservative 9; Mismatches 13; Indels 4; Gaps 1;

QY 4 KPNRPSNTVLPYQTPRLRDHYLLKGLGQGFQGTLYLCTEKSTSANYSACKSIPIKR 63
DB 3 KPNRPSNTVLPYQTPRLRDHYLLKGLGQGFQGTLYLCTEKSTSANYSACKSIPIKR 62

QY 64 CREDYEDVWEIQTIMHLSHPNVRKGTYESVVFHIVMEVCEGGELFDRIVSKGHS 123
DB 63 CREDYEDVWEIQTIMHLSHPNVRKGTYESVVFHIVMEVCEGGELFDRIVSKGHS 122

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QY 124 EREAVKLIITLGVVEACHSLGVWHRDLKPNFLDPSKODAKLKATDFGLSVFYKPGQY 183
 DB 123 EREAAKLIITLGVVEACHSLGVWHRDLKPNFLDPSKODAKLKATDFGLSVFYKPGQY 182
 QY 184 LVDVGSPPYVAPVVKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFQIILQGLK 243
 DB 183 LVDVGSPPYVAPVVKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFQIILQGLK 242
 QY 244 DFKSDPWTISBAADLIYKMLERSPKKRI SAHEALCHPMIVDEQAAPDKPLDPAVLSRL 303
 DB 243 DFKSDPWTISBAADLIYKMLERSPKKRI SAHEALCHPMIVDEQAAPDKPLDPAVLSRL 302
 QY 304 KQPSQWKKI KVALRVIAERLSEEEIGGLKELFKMIDTDSNGTITTFBELKAGLRKVGSEL 363
 DB 303 KQPSQWKKI KVALRVIAERLSEEEIGGLKELFKMIDTDSNGTITTFBELKAGLRKVGSEL 362
 QY 364 MESEIKSLMDAADIDNSGTIDYGEFLAATLHNMKEREELVLAFAFSDKDGSGYITIDE 423
 DB 363 MESEIKSLMDAADIDNSGTIDYGEFLAATLHNMKEREELVLAFAFSDKDGSGYITIDE 422
 QY 424 LQACTEFLGLDTPDDMIKEIDLNDGKIDFSEFTAMRKGDGVGRSRMTMKNLNFNIA 483
 DB 423 LQACTEFLGLDTPDDMIKEIDLNDGKIDFSEFTAMRKGDGVGRSRMTMKNLNFNIA 482
 QY 484 DAFGVGDG----EKSD 495
 DB 483 EAFGVEDTSTAKSD 498

RESULT 5

O24430 PRELIMINARY; PRT; 490 AA.
 ID O24430
 AC O24430
 DT 01-JAN-1998 (TREMELrel. 05, Created)
 DT 01-JAN-1998 (TREMELrel. 05, Last sequence update)
 DT 01-MAR-2002 (TREMELrel. 20, Last annotation update)
 DE Calmodulin-like domain protein kinase isoenzyme beta.
 OS Glycine max (Soybean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 OX NCBI_TaxID=3847;
 OX [1]
 RP SEQUENCE FROM N.A.
 RA McKendree W.L., Doostdar H., McColm T.G., Mayer R.T.;
 RT "cDNA cloning and expression of a gene (Accession No. 297064) from
 RT citrus paradisi roots similar to bacterial rRNA and HEA10 proteins
 RT and an mRNA from Brassica oleracea that is wound and dark inducible
 RT (PGR97-127).";
 RL Plant Physiol. 115:314-314 (1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Lee J.-Y., Yoo B.-C., Harmon A.C.;
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY, BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL; U69173; AAB80692.1; -;
 DR HSP; P02588; IPON.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR Pfam; PF00036; ehand; 4.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR ProDom; PD000012; EF-hand; 2.
 DR SMART; SM00054; EPH; 4.
 DR SMART; SM00220; S_TGK; 1.
 DR PROSITE; PS00018; EF HAND; UNKNOWN 4.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 490 AA; 55164 MW; 2333C411CAA43E0F CRC64;

Query Match 78.3%; Score 2030; DB 10; Length 490;
 Best Local Similarity 81.1%; Pred. No. 2.8e-141;
 Matches 386; Conservative 43; Mismatches 45; Indels 2; Gaps 2;
 QY 14 VLPYQTPRIURDHYLLGKLGQGGQFGTTVLCSTEKSTSNANYACKSIPKPKLVCRDYYDWR 73
 DB 12 VLPYQTPRIURDHYLLGKLGQGGQFGTTVLCSTEKSTSNANYACKSIPKPKLVCRDYYDWR 71
 QY 74 EIQIMHHLSEHNVRIRKGTVEYDSVFVHVMVECGEGELFDRIIVSKGHPSEERAVKLIKT 133
 DB 72 EIQIMHHLSEHNVRIRKGTVEYDSVFVHVMVECGEGELFDRIIVSKGHPSEERAVKLIKT 131
 QY 134 ILGVVEACHSLGVWHRDLKPNFLDPSKODAKLKATDFGLSVFYKPGQYLYDVVGSPPY 193
 DB 132 ILGVVEACHSLGVWHRDLKPNFLDPSKODAKLKATDFGLSVFYKPGQYLYDVVGSPPY 191
 QY 194 VAPELVKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFRQILQGLKDFKSDPWTI 253
 DB 192 VAPELVKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFRQILQGLKDFKSDPWTI 251
 QY 254 SEAAKOLIYKMLERSPKKRI SAHEALCHPMIVDEQAAPDKPLDPAVLSRLKQPSQWKKI 313
 DB 252 SEAAKOLIYKMLERSPKKRI SAHEALCHPMIVDEQAAPDKPLDPAVLSRLKQPSQWKKI 310
 QY 314 KVALRVIAERLSEEEIGGLKELFKMIDTDSNGTITTFBELKAGLRKVGSELSEIKSLMD 373
 DB 311 KVALRVIAERLSEEEIGGLKELFKMIDTDSNGTITTFBELKAGLRKVGSELSEIKSLMD 370
 QY 374 AADIDNSGTIDYGEFLAATLHNMKEREELVLAFAFSDKDGSGYITIDELOQACTEFL 433
 DB 371 AADIDNSGTIDYGEFLAATLHNMKEREELVLAFAFSDKDGSGYITIDELOQACTEFL 430
 QY 434 CDTFLDMDIKEIDLNDGKIDFSEFTAMRKGD-GVGRSRMTMKNLNFNIAADFGV 488
 DB 431 GDVHLDMEIKEDQNDGRIIDYAEFAAMKKGDPNMGSRMTMKNLNFNIAADFGM 486

RESULT 6

O24430 PRELIMINARY; PRT; 496 AA.
 ID O24430
 AC O24430
 DT 01-DEC-2001 (TREMELrel. 19, Created)
 DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMELrel. 20, Last annotation update)
 DE Calcium dependent protein kinase.
 DE RICDPK2.
 OS Solanum tuberosum (Potato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4113;
 OX [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN-CV, RISHIRI; TISSUE=CELL SUSPENSION;
 RA Puruchi N., Okita T., Hara N.;
 RT "Calcium dependent protein kinase genes from resistant and susceptible
 RT potato cultivars to Phytophthora infestans.";
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB051809; BAB63464.1; -;
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00036; ehand; 4.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR ProDom; PD000012; EF-hand; 2.
 DR SMART; SM00219; Tyrc; 1.
 DR PROSITE; PS00018; EF HAND; UNKNOWN 4.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN 1.
 DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00108; PROTEIN KINASE ST; UNKNOWN 1.
 KW ATP-binding; Kinase; Transferase.

SQ SEQUENCE 496 AA; 55774 MW; EC41F7AED33B6DD5 CRC64;

Query Match 76.0%; Score 1969.5; DB 10; Length 496;
 Best Local Similarity 76.6%; Pred. No. 8.3e-137;
 Matches 377; Conservative 55; Mismatches 53; Indels 7; Gaps 4;

QY 1 METKP--NPRRSNTVLPYQTPRLDRHYLLGKLGQGFQGTLYLCTEKSSTANYACKSIP 58
 DB 1 MEKPATPEKKSVMVLPYKTSQSLQSLTYTIGKLGQGFQGTLYLCTEKSSTANYACKSIP 60

QY 59 KRLVCREDEYDWRBQIOMHLSHPNVVRIGTYESVFIHMEVCEGGEFDRIVS 118
 DB 61 KKLICKEDYEDVWKEIQIMHLSHPNVVRIGTYEDALYVHIMELCAGGEFDRIVE 120

QY 119 KHFSREBAVKLITILGVVEACHSLGVWHRDLKPNFLFDSPKDKAKLKATDGLSVFY 178
 DB 121 KHYSREBAKLTITVGVVEACHSLGVWHRDLKPNFLFDSDEDAKATDGLSVFY 180

QY 179 KPGQYLYDVGVSPYVAPVLLKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFRQI 238
 DB 181 KPGETSDVGVSPYVAPVLLKCYGHESDVWSAGVILYLLSGVPPFWAETDMGIFRQI 240

QY 239 LQGLDFKSDPWTITSEAAKDLIYKMLSPKRSISAEALCHPWIVDEQAAPDKPLDPA 298
 DB 241 LRGLDLSEFPWGISDSAKDLIRKILDRNPKRLTAHEVLCHPWIVDTPVAPDKPLDSA 300

QY 299 VLRLKQFSOMNKKKVALRVIAERLSEEEIGGLKELFKMIDTDSNGTITPEELKAGLR 358
 DB 301 VLRLKQFSANMKKKVALRVIAERLSEEEIGGLKELFKMIDTDSNGTITPEELKEGLR 360

QY 359 VGSSELMESEIKSLMDAADIDNSGTIDYGEFLAATLHMNKMEREELVAAPSFDDKGGY 418
 DB 361 VGSSELMESEIKOLMDAADIDNSGTIDYGEFLAATLHMNKLEREENLLSAFSDKGGY 420

QY 419 ITDELQSACTEFLCDTPDDMKIDLDNDGKIDFSEFTAMRKGDG--VGRSRTWVK 476
 DB 421 ITBELQQAQCKEFLSELNDELKIDQNDGQIDYKEFSAMWRKGTGAVGR-RTIN 479

QY 477 NLNFIADAFGV 488
 DB 480 NL--NLGEALGL 489

RESULT 7

Q42396 Q42396 PRELIMINARY; PRT; 490 AA.
 AC Q42396;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Calcium-dependent protein kinase.
 GN CDPK9.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RA Hong Y., Takano M., Liu C.M., Gasch A., Chye M.L., Tan C.T., Koh C.C.,
 RA Chua N.H.;
 RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RX MEDLINE=20181125; PubMed=10718197;
 RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence
 RT features of the regions of 3,076,755 bp covered by sixty P1 and TAC
 RT clones.";
 RL DNA Res. 7:31-63 (2000).

CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL; U20626; AAA67657.1; -;
 DR EMBL; U20388; AAA67653.1; -;
 DR EMBL; AB025633; BAA97242.1; -;
 DR HSSP; P02588; 1PON.
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR Pfam; PF00036; sfhand; 4;
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR ProDom; PD000012; EF-hand; 2.
 DR SMART; SMO0054; EFh; 4.
 DR SMART; SMO0220; S_TKc; 1.
 DR PROSITE; PS00018; EF_HAND; UNKNOWN 4.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 490 AA; 55379 MW; 0315346396585264 CRC64;

Query Match 71.1%; Score 1844.5; DB 10; Length 490;
 Best Local Similarity 73.1%; Pred. No. 1.3e-127;
 Matches 553; Conservative 55; Mismatches 68; Indels 7; Gaps 2;

QY 1 METKPNRRPSNTVLPYQTPRLDRHYLLGKLGQGFQGTLYLCTEKSSTANYACKSIPKR 60
 DB 1 MANKPRTR----WLPYKTNVEDNYFLGVLGQGFQGTFLCTHKTGQKLACKSIPKR 56

QY 61 KLVCREDEYDWRBQIOMHLSHPNVVRIGTYESVFIHMEVCEGGEFDRIVSKG 120
 DB 57 KLLCQEDYDDVLRREIQIMHLSHPNVVRIGTYESVFIHMEVCEGGEFDRIVKRG 116

QY 121 HFSEBAVKLITILGVVEACHSLGVWHRDLKPNFLFDSPKDKAKLKATDGLSVFKP 180
 DB 117 HYSEREAALKITVGVVEACHSLGVWHRDLKPNFLFDSDEDAKSTDFGLSVFCTP 176

QY 181 GOVLYDVGVSPYVAPVLLKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFRQILQ 240
 DB 177 GEAFSELVGSAYVVAPEVLHKGYPGECVWSAGVILYLLCGFPFWAESIGIFRKLQ 236

QY 241 GLDFKSDPWTITSEAAKDLIYKMLSPKRSISAEALCHPWIVDEQAAPDKPLDPAVL 300
 DB 237 GKLEFEINPWPISSESADLIKKMLESNPKRLTAHVLCHPWIVDDKVPDKPLDCAV 296

QY 301 SRLKQFSQNKIKKVALRVIAERLSEEEIGGLKELFKMIDTDSNGTITPEELKAGLRVG 360
 DB 297 SRLKQFSANMKKKVALRVIAERLSEEEIGGLKELFKMIDTDSNGTITPEELKDSMRVG 356

QY 361 SELMESEIKSLMDAADIDNSGTIDYGEFLAATLHMNKMEREELVAAPSFDDKGGYIT 420
 DB 357 SELMESEIQELRAADVDSGTIDYGEFLAATLHMNKLEREENLLVAAPSFDDKGGYIT 416

QY 421 IDELQSACTEFLCDTPDDMKIDLDNDGKIDFSEFTAMRKGDGGRS---RTWKN 477
 DB 417 IEELQQAQCKEFLSELNDELKIDQNDGQIDYGEFVAMWRKNGTGGGIGRATMRNS 476

QY 478 LNF 480
 DB 477 LNF 479

RESULT 8

Q42396 Q42396 PRELIMINARY; PRT; 551 AA.
 AC Q42396;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE OSCDPK7.
 GN OSCDPK7.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 CC Eriarthoideae; Cryzeae; Oryza.
 CX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV, NIPPONBARE;
 RX MEDLINE=20387027; PubMed=10929125;
 RA Saijo Y., Hata S., Koyzuka J., Shimamoto K., Izui K.;
 RT "Over-expression of a single Ca2+-dependent protein kinase confers
 both cold and salt/drought tolerance on rice plants.";
 RL Plant J. 23:319-327(2000).
 DR EMBL; AB042550; BAB16888.1; -;
 DR HSSP; P02593; 1CTR.
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00036; ehand; 4.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR ProDom; PD000012; EF-hand; 2.
 DR SMART; SM00054; EFh; 4.
 DR SMART; SM00220; S_TKc; 1.
 DR SMART; SM00219; TyrKc; 1.
 DR PROSITE; PS00018; EF_HAND; UNKNOWN 3.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; transferase.
 SQ SEQUENCE 551 AA; 60966 MW; E479A089EF287A7B CRC64;

Query Match 69.4%; Score 1773; DB 10; Length 551;
 Best Local Similarity 71.2%; Pred. No. 2.9e-122;
 Matches 339; Conservative 53; Mismatches 82; Indels 2; Gaps 2;
 QY 13 TVLPYOTPLRDLHYLLGKLGQGGTGYLTCTEKSSTANYACKSIKRLVCKREDYEDVW 72
 DB 75 SVLGHTTPNLRDLVYALGRKLGQGGTGYLTCTELSTGVYACKSISKRLITKEDYEDV 134
 QY 73 REIQIMHLSSEHPNVVRIKGTVEDSVFVHIVVEYCEGGELFDRIIVSKGHFSEAEVKKIK 132
 DB 135 REIQIMHLSGHKNVVAIKGAYEDQVYVHIVMELCAGGELFDRIIQRGHYSEKAAALTR 194
 QY 133 TLGVVEACHSLGVHWRDLKPNELFDSPKDDAKLKATDFGLSVFYKPGQVLYDVVGSYP 192
 DB 195 IIVGVVEACHSLGVHWRDLKPNELFLANKDDLSLKALDFGLSVFFKPGQTFDVGSPY 254
 QY 193 YVAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFRQILQKGLDFKSDPWP 252
 DB 255 YVAPEVLKHYGEADVNTAGVILYLLSGVPPFWAETEQQGIQIFDAVLKGFIDFSDPWPV 314
 QY 253 ISBAKDLTYKMLERSPKKRISAHEALCHPMIVDEQAAPDKPLDPAVLRLKQFSOMNKKI 312
 DB 315 ISBAKDLTYKMLNRPKRELTAHEVLCHPMIRDHGVAPDRPLDPAVLRLKQFSOMNKKL 374
 QY 313 KQALRVIAERLSEBIEIGLKFPMIDTDSNGTITFEELKAGLRKRVGSELMSEIKSLM 372
 DB 375 KQALRVIAERLSEBIEIGLKFPMIDTDSNGTITFEELKAGLRKRVGSELMSEIKSLM 434
 QY 373 DAADINDSGTIDYGEFLAATLHMKNKEREELIVAAFSDFDKDGSYITIDELQSACTEFG 432
 DB 435 DAADINDSGTIDYGEFLAATLHMKNKEREELIVAAFSDFDKDGSYITIDELQSACTEFG 494
 QY 433 LCOTPLDDMKETDLNDGKIDFSEFTAMRKGD-GVGRSTWKNLNFNIAAFG 487
 DB 495 MPDAFLDDVINEAQDNDGRIDYGBFVAVMTKGNVGVGR-RTMNSNLNIMRDAPG 549
 RESULT 9
 ID 004417 PRELIMINARY; PRT; 492 AA.
 AC 004417;
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)

DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Calcium dependent protein kinase.
 GN ZMCDPKL.
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
 OC Panicoideae; Andropogoneae; Zea.
 ON NCBI_TaxID=4577;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HONEY BANTUM;
 RA Berberich T., Kusano T.;
 RT "Cycloheximide induces a subset of low-temperature-inducible genes in
 maize.";
 RL Mol. Gen. Genet. 0:0-0(1996).
 RP [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HONEY BANTUM;
 RX MEDLINE=97294505; PubMed=9150261;
 RA Berberich T., Kusano T.;
 RT "Cycloheximide induces a subset of low temperature-inducible genes in
 maize.";
 RL Mol. Gen. Genet. 254:275-283(1997).
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL; D84408; BAA12338.1; -;
 DR HSSP; P02593; 1CTR.
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR Pfam; PF00036; ehand; 4.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR ProDom; PD000012; EF-hand; 2.
 DR SMART; SM00054; EFh; 4.
 DR SMART; SM00220; S_TKc; 1.
 DR PROSITE; PS00018; EF_HAND; UNKNOWN 4.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 492 AA; 54734 MW; 8615C3C360CE949 CRC64;
 Query Match 67.6%; Score 1752; DB 10; Length 492;
 Best Local Similarity 70.6%; Pred. No. 8.7e-121;
 Matches 334; Conservative 54; Mismatches 83; Indels 2; Gaps 2;
 QY 13 TVLPYOTPLRDLHYLLGKLGQGGTGYLTCTEKSSTANYACKSIKRLVCKREDYEDVW 72
 DB 14 SVLGHTTPNLRDLVYALGRKLGQGGTGYLTCTELATGIDYACKSISKRLITKEDYEDV 73
 QY 73 REIQIMHLSSEHPNVVRIKGTVEDSVFVHIVVEYCEGGELFDRIIVSKGHFSEAEVKKIK 132
 DB 74 REIQIMHLSGHKNVVAIKGAYEDQVYVHIVMELCAGGELFDRIIQRGHYSEKAAALTR 133
 QY 133 TLGVVEACHSLGVHWRDLKPNELFDSPKDDAKLKATDFGLSVFYKPGQVLYDVVGSYP 192
 DB 134 IIVGVVEACHSLGVHWRDLKPNELFLANKDDLSLKALDFGLSVFFKPGQTFDVGSPY 193
 QY 193 YVAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFRQILQKGLDFKSDPWP 252
 DB 194 YVAPEVLKHYGEADVNTAGVILYLLSGVPPFWAETEQQGIQIFDAVLKGFIDFSDPWPV 253
 QY 253 ISBAKDLTYKMLERSPKKRISAHEALCHPMIVDEQAAPDKPLDPAVLRLKQFSOMNKKI 312
 DB 254 ISBAKDLTYKMLNRPKRELTAHEVLCHPMIRDHGVAPDRPLDPAVLRLKQFSOMNKKL 313
 QY 313 KQALRVIAERLSEBIEIGLKFPMIDTDSNGTITFEELKAGLRKRVGSELMSEIKSLM 372
 DB 314 KQALRVIAERLSEBIEIGLKFPMIDTDSNGTITFEELKAGLRKRVGSELMSEIKSLM 373
 QY 373 DAADINDSGTIDYGEFLAATLHMKNKEREELIVAAFSDFDKDGSYITIDELQSACTEFG 432

Db 374 DAADINSGTIDYIEFIAATLHNLKREHILVAAPSYFDKDGSGYITVDLQACKHN 433
QY 433 LCPDPTDDMIKIDLDNDGKIDFSEFTAMWRKGD-GVGRSRTMMKNLNFNIAD 484
Db 434 MPDAFLDDVINEADQNDGRIDYGEFVAMTKGNMGVR-RTMRNSLNSMRD 485
RESULT 10
Q43676 PRELIMINARY; PRT; 487 AA.
AC Q43676;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-VAR-2002 (TReMBLrel. 20, Last annotation update)
DE Calcium dependent protein kinase.
GN CDPK.
OS Phaseolus aureus (Mung bean) (Vigna radiata).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
OX NCBI_TaxID=3916;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=RWILCZ, AND CV. BERKEN; TISSUE=ETIOLATED HYPOCOTYL;
RX MEDLINE=96311003; PubMed=8704124;
RA Botella J.R., Arteca J.M., Somodevilla M., Arteca R.N.;
RT "Calcium-dependent protein kinase gene expression in response to
RT physical and chemical stimuli in mungbean (Vigna radiata).";
RL Plant Mol. Biol. 30:1129-1137(1996).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; U08140; AAC49403.1; -.
DR HSSP; Q63450; 1A06.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00036; ehand; 4.
DR Pfam; PF00089; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 1.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 4.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00018; EF HAND; UNKNOWN 4.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 487 AA; 54700 MW; 54E6FBF5D93AEB2 CRC64;
Query Match 67.5%; Score 1751; DB 10; Length 487;
Best Local Similarity 69.1%; Pred. No. 1e-120;
Matches 327; Conservative 64; Mismatches 80; Indels 2; Gaps 2;
QY 14 VLPVQTPRLRDHYLLGKLGQGGQFGTTVLTCTEKSANYACKSIPIKRLVCREDYEDVWR 73
Db 12 VLGHKTPNIRDLYTLGRKLGQGGQFGTTVLTCTENSTSEYACKSISKEKLISKEDVEDVRR 71
QY 74 EIQIMHLSHPNVVRIKGTVEDSVFVHIVMEVCEGELFDRIVSKGHFSEREAVKLTK 133
Db 72 EIQIMHLSHAGNHNVTIKGAYEDFVHIVMELCGGELFDRIIQRGHYTERKAELTKI 131
QY 134 ILGVVEACHSLGVWHRDLKPNFLDSEFKDDAKLKATDFGLSVFYKPGQYLYDVVGSPPY 193
Db 132 IVGVVEACHSLGVWHRDLKPNFLVNKDDDFSLKATDFGLSVFFKPGQIFTDVVGSPY 191
QY 194 VAPVVKCYGPEIDVWSAGVILYLLSGVPFWAETESGIFRQILQGLKDFKSDPWPFI 253
Db 192 VAPVLLKHGPEADVMTAGVILYLLSGVPFWAETQGGIFDAVLKGVDFDSDPWPFI 251
QY 254 SEAAKDLIYKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAVLRLKQFSQMNKIK 313
Db 252 SUGKDLTKMLCSQPSERLTAHQVLCHPWICENGVAFDRAIDPAVLRLKQFSQMNKIK 311
QY 314 KVALRVIAERLSEEBEIGGLKELFKWIMDTDNGSTTTFBELKAGLRVGSSELMSEIKSLMD 373

Db 312 KVALVIAERLSEEBEIGGLKELFKWIMDTDNGSTTTFBELKAGLRVGSSTLKVDVEIRLME 371
QY 374 ADINSGTIDYGEFLAATLHNLKREHILVAAPSYFDKDGSGYITVDLQACKHN 433
Db 372 AADVDSGTIDYGEFLAATLHNLKREHILVAAPSYFDKDGSGYITVDLQACKHN 431
QY 434 CDTPLDDMIKIDLDNDGKIDFSEFTAMWRKGD-GVGRSRTMMKNLNFNIAD 485
Db 432 TDAFLDIIIREVDQNDGRIDYGEFVAMTKGNMGVR-RTMRNSLNSMRD 483
RESULT 11
O04123 PRELIMINARY; PRT; 554 AA.
AC O04123;
DT 01-JUL-1997 (TReMBLrel. 04, Created)
DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
DT 01-VAR-2002 (TReMBLrel. 20, Last annotation update)
DE Calcium-dependent protein kinase.
OX Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=INBREED LINE H84;
RX MEDLINE=97201047; PubMed=9048876;
RA Saijo Y., Hata S., Sheen J., Izui K.;
RT "cDNA cloning and prokaryotic expression of a maize calcium-dependent
RT protein kinase."; Acta 1350:109-114(1997).
RL Biochim. Biophys. Acta 1350:109-114(1997).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; D87042; BAA13232.1; -.
DR HSSP; P02593; 1CTR.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00036; ehand; 4.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 1.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 4.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00018; EF HAND; UNKNOWN 4.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 554 AA; 61056 MW; 51FC6F44684C57C6 CRC64;
Query Match 67.3%; Score 1745; DB 10; Length 554;
Best Local Similarity 70.0%; Pred. No. 3.4e-120;
Matches 333; Conservative 57; Mismatches 84; Indels 2; Gaps 2;
QY 13 TVLPVQTPRLRDHYLLGKLGQGGQFGTTVLTCTEKSANYACKSIPIKRLVCREDYEDVWR 72
Db 78 SVLGHPTNRLDLYALGRKLGQGGQFGTTVLTCTLATGVYACKSISKRKLITREDVDDVR 137
QY 73 REIQIMHLSHPNVVRIKGTVEDSVFVHIVMEVCEGELFDRIVSKGHFSEREAVKLTK 132
Db 138 REIQIMHLSHAGNHNVTIKGAYEDQVYHIVMELCGGELFDRIIQRGHYTERKAELTK 197
QY 133 TILGVVEACHSLGVWHRDLKPNFLDSEFKDDAKLKATDFGLSVFYKPGQYLYDVVGSPPY 192
Db 198 IIVGVVEACHSLGVWHRDLKPNFLVNKDDDFSLKATDFGLSVFFKPGQIFTDVVGSPY 257
QY 193 YVAPVVKCYGPEIDVWSAGVILYLLSGVPFWAETESGIFRQILQGLKDFKSDPWPFI 252
Db 258 YVAPVLLKHGPEADVMTAGVILYLLSGVPFWAETQGGIFDAVLKGVDFDSDPWPFI 317
QY 253 ISEAAKDLIYKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAVLRLKQFSQMNKIK 312

SQ SEQUENCE 578 AA; 64779 MW; 1009FF973EB662D2 CRC64;
 Query Match 67.1%; Score 1739.5; DB 10; Length 578;
 Best Local Similarity 67.6%; Pred. No. 9.3e-120;
 Matches 326; Conservative 62; Mismatches 79; Indels 15; Gaps 1;

QY 2 ETKNPRRP-----SNTVLPYQTPLRDHYLLGKLGQGGFGTTLCTEK 46
 DB 75 EEKEQPKPKPKPAEMKRVSSAGRLTDSVLQKTKGNLKEFFSIGKLGQGGFGTTFKCVEX 134
 QY 47 STSANYACKSIPKRLKLVCREDEYDWMREIQIMHHLSEHPNVVRIKGTYESVFIHMEV 106
 DB 135 ATGKEYACKSIKAKRLTDDDDVEDVRREVQIMHHLAGHPHVISIKGAYEDAVAVHVMF 194
 QY 107 CEGGELFDRIIVSKGHPSEBAVKLITKILGVVEACHSLGVNHRDLKPNFLFDPKDDAK 166
 DB 195 CAGGELFDRIIQRGHYTERKAAELTRTIIVGVVEACHSLGVNHRDLKPNFLFVDQKEDSL 254
 QY 167 LKATDFGLSVFVKPGQYLVDVVGSPYVVAPEVLKCYGPEIDVMSAGVILYLLSGVPPF 226
 DB 255 LKATDFGLSIFPKGDRFTDVVGSPYVVAPEVLKRYGPEADVMSAGVILYLLSGVPPF 314
 QY 227 WAETSGIFRQILQKLPKSDPWTITSEAAKDLIYKMLERSPKKRISAHEALCHPWIVD 286
 DB 315 WAENEOGIEFQVLHGDLDPKSDPNPISSEDARKDLRRMLVRDPRRLTAHEVLCHPWVQV 374
 QY 287 EQAAPDKPLDPAVLARLKFQFQSNKIKKMLARVIAERLSEEEIGLKEFLPMIDTNSGT 346
 DB 375 DGVAPEKPLDSAVLSRMKQFSAMNKLKMLARVIAESLSEEEIAGLKEMFKMTDTSNGQ 434
 QY 347 ITFEELKAGLRVSGELMESEIKSLMDAADINSQTIYGFELATLHMNMVREELIVA 406
 DB 435 ITFEELKEGLKRFSGNLKETEYIDLMQAADVNSGTIDYGEFIAATLHMNKIERQDLHFA 494
 QY 407 AFSDFDKDGSGYITIDELQASCTEFLGCLDTPDDMIKETDLDNDGKIDFSEFTAMRKGD 466
 DB 495 APCYFDKDGSGYITADELQACBEEFGIDVRMEEMIREADQNDGRIDINEFVAMMQGN 554
 QY 467 GV 468
 DB 555 PV 556

RESULT 14
 Q93YF3 PRELIMINARY; PRT; 578 AA.
 ID Q93YF3
 AC Q93YF3
 DT 01-DEC-2001 (T-EMBLrel. 19, Created)
 DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (T-EMBLrel. 20, Last annotation update)
 DE Calcium-dependent protein kinase 3.
 GN CDPK3.
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID=4097;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=21481752; PubMed=11597999;
 RX Romeis T., Ludwig A.A., Martin R., Jones J.D.G.;
 RT "Calcium-dependent protein kinases play an essential role in a plant
 defence response".
 RL ENBO J. 20:5558-5567(2001).
 DR EMBL; AJ344155; CAC82999.1;
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR Pfam; PF00036; ehand; 4
 DR Pfam; PF00069; pkinase; 1
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR ProDom; PD000012; EF-hand; 2.
 DR PROSITE; PS00018; EF_HAND; UNKNOWN_4.

DR PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN_1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
 KW ATP-binding; Kinase; Transferase.
 SQ SEQUENCE 578 AA; 64779 MW; 88778B73F85A16B6 CRC64;

Query Match 66.9%; Score 1733.5; DB 10; Length 578;
 Best Local Similarity 67.4%; Pred. No. 2.6e-119;
 Matches 325; Conservative 62; Mismatches 80; Indels 15; Gaps 1;

QY 2 ETKNPRRP-----SNTVLPYQTPLRDHYLLGKLGQGGFGTTLCTEK 46
 DB 75 EEKEQPKPKPKPAEMKRVSSAGRLTDSVLQKTKGNLKEFFSIGKLGQGGFGTTFKCVEX 134
 QY 47 STSANYACKSIPKRLKLVCREDEYDWMREIQIMHHLSEHPNVVRIKGTYESVFIHMEV 106
 DB 135 ATGKEYACKSIKAKRLTDDDDVEDVRREVQIMHHLAGHPHVISIKGAYEDAVAVHVMF 194
 QY 107 CEGGELFDRIIVSKGHPSEBAVKLITKILGVVEACHSLGVNHRDLKPNFLFDPKDDAK 166
 DB 195 CAGGELFDRIIQRGHYTERKAAELTRTIIVGVVEACHSLGVNHRDLKPNFLFVDQKEDSL 254
 QY 167 LKATDFGLSVFVKPGQYLVDVVGSPYVVAPEVLKCYGPEIDVMSAGVILYLLSGVPPF 226
 DB 255 LKATDFGLSIFPKGDRFTDVVGSPYVVAPEVLKRYGPEADVMSAGVILYLLSGVPPF 314
 QY 227 WAETSGIFRQILQKLPKSDPWTITSEAAKDLIYKMLERSPKKRISAHEALCHPWIVD 286
 DB 315 WAENEOGIEFQVLHGDLDPKSDPNPISSEDARKDLRRMLVRDPRRLTAHEVLCHPWVQV 374
 QY 287 EQAAPDKPLDPAVLARLKFQFQSNKIKKMLARVIAERLSEEEIGLKEFLPMIDTNSGT 346
 DB 375 DGVAPEKPLDSAVLSRMKQFSAMNKLKMLARVIAESLSEEEIAGLKEMFKMTDTSNGQ 434
 QY 347 ITFEELKAGLRVSGELMESEIKSLMDAADINSQTIYGFELATLHMNMVREELIVA 406
 DB 435 ITFEELKDGKSGYITIDELQASCTEFLGCLDTPDDMIKETDLDNDGKIDFSEFTAMRKGD 466
 DB 495 APCYFDKDGSGYITADELQACBEEFGIDVRMEEMIREADQNDGRIDINEFVAMMQGN 554
 QY 467 GV 468
 DB 555 PV 556

RESULT 15
 Q38872 PRELIMINARY; PRT; 544 AA.
 ID Q38872
 AC Q38872
 DT 01-NOV-1996 (T-EMBLrel. 01, Created)
 DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
 DT 01-MAR-2002 (T-EMBLrel. 20, Last annotation update)
 DE Calmodulin-domain protein kinase CDPK isoform 6.
 GN CPK6 OR F5J6.5.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC euroids I; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strain=COLUMBIA;
 RX Krabak E.M., Dickmann L.J., Satterlee J.S., Sussman M.R.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA STRAIN=CV. COLUMBIA;
 RX Zhong J.M., Ma P.N., Parnell L.D., Chen C.-N., Chen E.Y.;
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.


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RC STRAIN=CV. COLUMBIA;
RA Parnell L., McCombie W.R.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
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RC STRAIN=CV. COLUMBIA;
RA Zhong J.M., Ma P.N., Parnell L.D., Chen C.-N., Chen E.Y.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Parnell L.,
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; U31835; AAB03246.1; -.
DR EMBL; AC002329; AAB86506.1; -.
DR HSSP; P02593; 1CTR.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00036; ehand; 4.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 1.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 4.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_4.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding, Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 544 AA; 61111 MW; EA4F047BEE985E4F CRC64;

Query Match 66.8%; Score 1731; DB 10; Length 544;
Best Local Similarity 68.3%; Pred. No. 3.6e-119;
Matches 326; Conservative 65; Mismatches 85; Indels 2; Gaps 2;

QY 6 NPREFNTVLFPYQTPRLDRHYLLGKLGQCGFTTYLCTEKSTSANACKSIPKRLVCR 65
DB 65 NVDNQSYVVLGHKTPNIRDLYTLRSKLGQCGFTTYLCTDIATGVDYACKSISKRLISK 124

QY 66 EDYEDVWREIQIMHLSHNPVRIKGTVEDSVFVHVMVEVCEGGELFDRIVSKGHFSER 125
DB 125 EDVEDVAREIQIMHLAGHKNIVTIKAGYEDPLVHVMELCAGGELFDRIRHGHYSER 184

QY 126 EAVKLIKITLGVWEACHSLGVMHRDLKPNFLFDSPKDDAKLKATDFGLSVFYKPGQYLY 185
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QY 186 DVGSPYTVAPVVLKCVGPIDVWAGVILYILLSGVPPFWAETESGIFRQILQKLDLF 245
DB 245 DVGSPYTVAPVVLKHYGPEDVWAGVILYILLSGVPPFWAETESGIFRQILQKLDLF 304

QY 246 KSDPWTISEAAKDLIVKMLERSPKKRIISAHEALCHPMIVDEQAAPDKLPDPAVLSRLKQ 305
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Search completed: February 13, 2003, 21:10:41
Job time : 77 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 13, 2003, 17:41:47 ; Search time 4632 Seconds
(without alignments)
10976.382 Million cell updates/sec

Title: US-09-848-806-2

Perfect score: 1747

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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
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- 12: gb.sy.*
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- 15: em.ba.*
- 16: em.fun.*
- 17: em.hum.*
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- 32: em.htg_other.*
- 33: em.htg_mus.*
- 34: em.htg_pln.*
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- 38: em_sy.*
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- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1747	100.0	1747	8	ATHCDPKB
2	1711	97.9	1750	8	AY050981 Arabidops
3	1515.8	86.8	1519	8	AY113986 Arabidops
4	1202.4	68.8	1657	8	ATU31752 Arabidops
5	846.4	47.3	1754	8	GM069173 Arabidops
6	803.6	46.0	1732	8	AB051809 Arabidops
7	756.4	43.3	1768	6	AX077706 Sequence
8	756.4	43.3	1768	8	SOYCADPK
9	744.2	42.6	1693	8	ATACDPK9
10	712.6	40.8	2036	8	ATU31835 Arabidops
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15	666.2	38.1	158096	8	AC007887 Genomic s
16	666	38.1	2019	8	NTA344154 Arabidops
17	657.6	37.6	2270	8	AY072801 Cucurbita
18	652.6	37.4	2550	6	AX077715 Sequence
19	652.6	37.4	2550	8	CPU90262 Cucurbita p
20	652.2	37.3	1746	8	NBE344156 Arabidops
21	649.4	37.2	2126	8	AB042550 Oryza sat
22	649	37.1	2214	8	AY072802 Cucurbita
23	645	36.9	2214	8	ATHCALLIPR
24	643.4	36.8	1857	8	D84408 Maize mRNA
25	641.8	36.7	2142	8	ATU31833 Arabidops
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27	629.8	36.1	2022	8	VRU08140 Arabidops
28	625	35.8	2248	8	D87042 Vigna radia
29	619.4	35.5	2243	8	TRU82087 Arabidops
30	596.2	34.1	1041	8	AY030280 Arabidops
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40	551	31.5	2566	8	ZMA7366 Arabidops
41	543.6	31.1	1353	8	MZECDPK
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ALIGNMENTS

RESULT 1
ATHCDPKB

LOCUS
DEFINITION

Arabidopsis thaliana mRNA for calcium-dependent protein kinase
(CDPK), complete cds.
1747 bp mRNA linear PLN 05-FEB-1999

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi

REFERENCE

1 (bases 1 to 1747)

AUTHORS

Urao,T., Katagiri,T., Mizoguchi,T., Yamaguchi-Shinozaki,K.,

Hayashida, N. and Shinozaki, K.
Two genes that encode Ca(2+)-dependent protein kinases are induced
by drought and high-salt stresses in Arabidopsis thaliana
Mol. Gen. Genet. 244 (4), 331-340 (1994)
94359455
REFERENCE
2 (bases 1 to 1747)
Shinozaki, K.
Direct Submission
Submitted (30-OCT-1993) Kazuo Shinozaki, Tsukuba Life Science
Center, The Inst. of Physical and Chemical Res.; 3-1-1 Kohyadai,
Tsukuba, Ibaraki 350, Japan (E-mail: shinozaki@rics1.riken.go.jp,
Tel: 0298-36-4359, Fax: 0298-36-9060)
On Mar 22, 1996 this sequence version replaced gi:540482.

FEATURES

Location/Qualifiers

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EALCHPVIQEAAPKDPDPVLSRLKQFSQNKIKWALKVIAERLSEBEEIGLKE

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1747

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Matches 1747; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 181 ACAACCTATCTCTGACAGAGAAATCAACCTCGCCTAATTAACGCTGCAATCGATCCG 240

Db 181 ACAACCTATCTCTGACAGAGAAATCAACCTCGCCTAATTAACGCTGCAATCGATCCG 240

QY 241 AAGCGAAGCTCGTGTGCGGAGATTAACAGATCATGTGGCGTGAGATTCAGATCATG 300

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QY 1261 GAG 1320

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QY 1381 GACGACATGATCAAG 1440

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RESULT 2
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 DEFINITION (Atg35670) mRNA, complete cds.
 ACCESSION AY050981.1 GI:15293094
 VERSION
 KEYWORDS
 SOURCE Arabidopsis thaliana
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi
 1 (bases 1 to 1750)
 Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Chung,M.K.,
 Goldsmith,A.D., Lee,J.M., Quach,H.L., Toriumi,M., Yu,G., Bowser,L.,
 Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J.,
 Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Lam,B.,
 Lin,J., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T.,
 Satou,M., Seki,M., Shinn,P., Southwick,A., Shinozaki,K.,
 Davis,R.W., Ecker,J.R. and Theologis,A.
 Arabidopsis Full Length cDNA Clones
 Unpublished
 2 (bases 1 to 1750)
 Yamada,K., Liu,S.X., Pham,P.K., Banh,J., Banno,F., Dale,J.M.,
 Goldsmith,A.D., Jiang,P.X., Lee,J.M., Onodera,C.S., Quach,H.L.,
 Tang,C.C., Toriumi,M., Yamamura,Y., Yu,G., Yu,S., Bowser,L.,
 Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J.,
 Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C.,
 Koesema,E., Lam,B., Lin,J., Meyers,M.C., Miranda,M., Narusaka,M.,
 Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M., Shinn,P.,
 Southwick,A., Tracy,S.E., Shinozaki,K., Davis,R.W., Ecker,J.R. and
 Theologis,A.
 Direct Submission
 Submitted (07-AUG-2001) Plant Gene Expression Center, 800 Buchanan
 Street, Albany, CA 94710, USA
 RIKEN Genomic Sciences Center (GSC) members carried out the
 collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN
 Arabidopsis Full-length cDNA': Seki,M., Narusaka,M., Ishida,J.,
 Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
 Hayashizaki,Y. and Shinozaki,K.
 The Salk, Stanford, PGE (SSP) Consortium members carried out the
 sequencing and annotation of the RAFL cDNAs: Yamada,K., Liu,S.X.,
 Pham,P.K., Banh,J., Banno,F., Dale,J.M., Goldsmith,A.D.,
 Jiang,P.X., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C.,
 Toriumi,M., Yamamura,Y., Yu,G., Yu,S., Bowser,L., Chen,H.,
 Cheuk,R., Jones,T., Karlin-Neumann,G., Kim,C., Koesema,E., Lam,B.,
 Lin,J., Meyers,M.C., Miranda,M., Nguyen,M., Palm,C.J., Shinn,P.,
 Southwick,A., Tracy,S.E., Davis,R.W., Ecker,J.R. and Theologis,A.

Yamada,K. (SSP/PGE) and Seki,M. (RIKEN GSC) contributed equally to
 this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP/PGE)
 contributed equally to this work as PIs.

FEATURES

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VERSION U31752.1 GI:1399266
 KEYWORDS Arabidopsis thaliana.
 SOURCE Arabidopsis thaliana
 ORGANISM Arabidopsis thaliana
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 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 REFERENCE 1 (bases 1 to 1657)
 AUTHORS Hrabak, E.M., Dickmann, L.J., Satterlee, J.S. and Sussman, M.R.
 TITLE Characterization of eight new members of the calmodulin-like domain
 protein kinase gene family from Arabidopsis thaliana
 JOURNAL Plant Mol. Biol. 31 (2), 405-412 (1996)
 MEDLINE 96343943
 PUBMED 8756605
 REFERENCE 2 (bases 1 to 1657)
 AUTHORS Hrabak, E.M.
 TITLE Direct Submission
 JOURNAL Submitted (17-JUL-1995) Estelle M. Hrabak, Horticulture, University
 of Wisconsin, 1575 Linden Drive, Madison, WI 53706, USA
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kinase, complete cds.
ACCESSION
AB051809
VERSION
AB051809.1 GI:15289759
KEYWORDS
Solanum tuberosum (cultivar:Rishiri) cell suspension cDNA to mRNA,
clone_lib:potato cv. Rishiri cDNA.
ORGANISM
Solanum tuberosum
Solanum tuberosum
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
REFERENCE
1 Furuichi N., Okura T. and Hara N.
Calcium dependent protein kinase genes from resistant and
susceptible potato cultivars to Phytophthora infestans
Unpublished
2 (bases 1 to 1732)
Furuichi N. and Okura T.
Direct Submission
Submitted (25-NOV-2000) Nactaka Furuichi, Niigata university,
Agriculture; 2-8050, Igarashi, Niigata shi, Niigata Ken 950-2181,
Japan [E-mail:nfuruaga@niigata-u.ac.jp]
URL:ftp://www.niigata-u.ac.jp, Tel:81-25-262-7520 (ex.7520),
Fax:81-25-262-7520)
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ACCESSION AX077706
VERSION AX077706.1 GI:13122081
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SOURCE soybean.
ORGANISM Glycine max
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Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 1768)
REFERENCE Holt,C.D., White,A.J., Michael,A.J. and Osborn,R.W.
AUTHORS Herbicide resistant plants and methods for the production thereof
TITLE Patent: WO 0107592-A 13 01-FEB-2001;
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 DEFINITION M64987
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 VERSION calcium/calmodulin-dependent protein kinase.
 KEYWORDS Glycine max cDNA to mRNA.
 SOURCE Glycine max
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

REFERENCE 1 (bases 1 to 1768)
 AUTHORS Harper,J.F., Suesman,M.R., Schaller,G.E., Putnam-Evans,C., Charbonneau,H. and Harmon,A.C.
 TITLE A calcium-dependent protein kinase with a regulatory domain similar to calmodulin
 JOURNAL Science 252 (5008), 951-954 (1991)
 MEDLINE 91240279
 PUBMED 1852075

FEATURES
 source Location/Qualifiers
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RESULT 9
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DEFINITION complete cds.
ACCESSION U20388
VERSION U20388.1 GI:836937
KEYWORDS calcium dependent protein kinase.
SOURCE Arabidopsis thaliana
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 1693)
Hong, Y., Takano, M., Liu, C.M., Gasch, A., Chye, M.L. and Chua, N.H.
Expression of three members of the calcium-dependent protein kinase
Gene family in Arabidopsis thaliana (1996)
Plant Mol. Biol. 30 (6), 1259-1275
96311013
MEDLINE PUBMED
8704134
REFERENCE 2 (bases 1 to 1693)
Hong, Y.
Direct Submission
Submitted (27-JAN-1995) Yan Hong, Institute of Molecular and Cell
Biology, National University of Singapore, 10 Kent Ridge Crescent,
Singapore, Republic of Singapore, 0511
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

1 Furuichi,N., Okuta,T. and Hara,N.
Calcium dependent protein kinase genes from resistant and
susceptible potato cultivars to Phytophthora infestans
Unpublished
2 (Bases 1 to 2393)
Furuichi,N. and Okuta,T.
Direct Submission
JOURNAL
Submitted (25-NOV-2000) Naotaka Furuichi, niigata university,
Agriculture, 2-8050, Igarashi, Niigata shi, Niigata Ken 950-2181,
Japan (E-mail:nfuru@agr.niigata-u.ac.jp,
URL:http://www.niigata-u.ac.jp, Tel:81-25-262-7520(ex.7520),
Fax:81-25-262-7520)

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ACCESSION AJ344155
VERSION AJ344155.1 GI:16215470
KEYWORDS calcium-dependent protein kinase; cdpk3 gene.
SOURCE common tobacco.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asterales; euasterids I; Solanales; Solanaceae; Nicotiana.
1 Romeis, T., Ludwig, A.A., Martin, R. and Jones, J.D.
Calcium-dependent protein kinases play an essential role in a plant
defence response
EMBO J. 20 (20), 5556-5567 (2001)
21481752
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MEDLINE
PUBMED
2 (bases 1 to 2437)
Romeis, T.
Direct Submission
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BASE COUNT 581 a 351 c 466 g 569 t

Query Match 39.4%; Score 688.4; DB 8; Length 1967;

Best Local Similarity 67.2%; Pred. No. 1.7e-138;

Matches 974; Conservative 0; Mismatches 476; Indels 0; Gaps 0;

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RESULT 15

AC007887/c

LOCUS

DEFINITION

AC007887

AC007887

AC007887.9

GI:8778333

HTG.

KEYWORDS

SOURCE

ORGANISM

Arabidopsis thaliana.

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

1 (bases 1 to 158096)

Ecker, J.R.

Direct Submission

Submitted (22-JUN-1999)

Department of Biology, University of Pennsylvania, 38th Street and

Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA

2 (bases 1 to 158096)

Ecker, J.R.

Direct Submission

Submitted (04-OCT-1999)

Department of Biology, University of Pennsylvania, 38th Street and

Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA

3 (bases 1 to 158096)

Cheuk, R., Shinn, P., Brooks, S., Buehler, E., Chao, Q.,

Johnson-Hopson, C., Khan, S., Kim, C., Altafi, H., Bei, B., Chin, C.,

Chiou, J., Choi, E., Conn, L., Conway, A., Gonzalez, A., Hansen, N.,

Genomic sequence for Arabidopsis thaliana BAC F1504 from chromosome

linear

PLN 28-JUN-2000

Howing, B., Koo, T., Lam, B., Lee, J., Lenz, C., Li, J., Liu, A., Liu, J.,
 Liu, S., Mukharshy, N., Nguyen, M., Palm, C., Pham, P., Sakano, H.,
 Schwartz, J., Southwick, A., Thaveri, A., Toriumi, M., Vayenberg, M.,
 Yu, G., Davis, R., Federspiel, N., Theologis, A. and Ecker, J.
 Direct Submission
 Submitted (28-JUN-2000) Arabidopsis thaliana Genome Center,
 Department of Biology, University of Pennsylvania, 38th and
 Hamilton Walk, Philadelphia, PA 19104-6018, USA
 On Jun 28, 2000 this sequence version replaced gi:6007863.
 This submission of BAC F1504 is shorter by 1338 bases. The
 original BAC had a Tn10 transposon insertion
 (gb|J01829.1|FN10IS13) from E. coli located at the junction of
 bases 18229 and 18230 of this submission.

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CDS

CDS

CDS

CDS

CDS

CDS

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GenCore version 5.1.3
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DM nucleic - nucleic search, using sw model

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23: /SID32/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT.*
24: /SID32/gcgdata/geneseq/geneseqn-embl/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1747	100.0	1747	24	Arabidopsis CDPK2
2	1202.4	68.8	1657	24	Arabidopsis CDPK4
3	1183.2	67.7	1506	21	Arabidopsis thalia
4	756.4	43.3	1768	22	Soybean calcium de
5	688.4	39.4	1671	21	Arabidopsis thalia
6	652.6	37.4	2550	22	Cucurbita pepo cal
7	629.8	36.1	2022	22	Vigna radiata.calc
8	597.4	34.2	3054	21	Arabidopsis thalia
9	571.4	32.7	2334	22	Rice calcium depen

10	537.2	30.7	1910	22	AAF74275	Sweet potato calci
11	531.8	30.4	2230	24	ABA91081	Physcomitrella pat
12	523	29.9	1647	22	AAF74281	Liverwort calcium
13	522.8	29.9	1791	22	AAF74270	Carrot calcium dep
14	521.6	29.9	2363	22	AAF74284	Common ice plant c
15	520.2	29.8	2436	22	AAF74273	Soybean calcium de
16	515.6	29.5	2306	22	AAF74272	Maize calcium depe
17	513.4	29.4	1647	22	AAF74282	Liverwort calcium
18	512.6	29.3	2466	15	AAQ66397	Protein kinase cDN
19	509.4	29.2	1836	21	AAQ66397	Arabidopsis thalia
20	507.6	29.1	1723	22	AAF74271	Maize calcium depe
21	501	28.7	2040	22	AAF74278	Rice calcium depen
22	499.2	28.6	1392	21	AAQ66397	Arabidopsis thalia
23	496.8	28.4	2251	22	AAF74276	Tobacco calcium de
24	485.2	27.8	1761	21	AAQ66397	Arabidopsis thalia
25	481.2	27.5	2162	22	AAF74262	Arabidopsis thalia
26	478.2	27.4	1967	22	AAF74280	Strawberry calcium
27	448.2	25.7	455	24	ABL93806	Arabidopsis thalia
28	444.6	25.4	1726	22	AAF74263	Arabidopsis thalia
29	444.4	25.4	2087	22	AAF74266	Tobacco homolog of
30	405.8	23.2	1133	22	AAQ66397	Tobacco CDPK cDNA.
31	379.8	21.7	921	20	AAV22757	Nucleotide sequenc
32	346.2	19.8	1020	19	AAV36878	ATCDPK1A PK domain
33	346.2	19.8	1020	22	AA166819	Zea mays DNA fragm
34	337.6	19.3	1412	21	AAQ66397	Peanut calcium dep
35	326	18.7	956	22	AAF74269	Arabidopsis thalia
36	299	17.1	1781	21	AAQ66397	Human dithio polynu
37	290.6	16.6	798	24	ABK71570	Physcomitrella pat
38	277.8	15.9	1387	24	ABA91068	Potato calcium dep
39	257.2	14.7	2210	22	AAF74279	Arabidopsis thalia
40	227.4	13.0	955	24	ABN98558	Physcomitrella pat
41	221.6	12.7	2254	24	AAQ66397	Arabidopsis thalia
42	220.6	12.6	1785	21	AAQ66397	Arabidopsis thalia
43	204.6	11.7	2202	21	AAQ66397	Arabidopsis thalia
44	189.6	10.9	2374	22	AAH46398	Rice CDPK cDNA (cl
45	183.2	10.5	13114	21	AAQ66397	Rice Gene for resi

ALIGNMENTS

RESULT 1
ABA06021
ID ABA06021 standard; cDNA; 1747 BP.
XX ABA06021;
AC ABA06021;
DT 08-MAR-2002 (first entry)
DE Arabidopsis CDPK2 encoding polynucleotide SEQ ID NO 2.
XX Arabidopsis; CDPK2; CDPK4; calcium dependent protein kinase; oilseed;
KW disease resistance; agricultural; pathogen; crop yield; ornamental;
KW fungicide; bactericide; nematocide; insecticide; viricide; cereal;
KW transgenic; plant; enzyme; gene; ss.
XX Arabidopsis thaliana.
OS Arabidopsis thaliana.
FH Key Location/Qualifiers
CDS 67..1554
FT /*tag= a
FT /product= "CDPK2"
XX WO200184911-A1.
XX 15-NOV-2001.
XX 04-MAY-2001; 2001WO-US14368.
XX 05-MAY-2000; 2000US-201925P.
XX (GEO) GEN HOSPITAL CORP.
XX

PI Sheen J;
XX WPI; 2002-062179/08.
DR P-PSDB; AAM48000.
XX
XX Producing plant having increased disease resistance, comprises
PT regenerating plant from a non-naturally occurring plant cell
PT over-expressing a polynucleotide encoding a calcium dependent protein
PT kinase polypeptide -
XX
XX Disclosure; Fig 1; 44pp; English.
XX
XX The invention relates to producing a plant having increased disease
CC resistance, comprising providing a non-naturally occurring plant cell
CC over-expressing a polynucleotide encoding a calcium dependent protein
CC kinase (CDPK) polypeptide and regenerating a plant from the plant
CC cell, where the CDPK polypeptide is expressed in the plant, increasing
CC the resistance of the plant to disease as compared to a
CC naturally-occurring plant. The method is useful for a variety of
CC agricultural and commercial purposes including improving a plant's
CC resistance against plant pathogens, increasing crop yields, improving
CC crop and ornamental quality and reducing agricultural production costs.
CC The method facilitates an effective and economical method for in-plant
CC protection against plant pathogen, reducing or minimising the need for
CC traditional chemical practices (e.g. application of fungicides, insecticides,
CC bactericides, nematocides, insecticides, or viricides) that are typically
CC used by farmers for controlling the spread of plant pathogens and
CC providing protection against disease causing pathogens. The method
CC contributes to the production of high quality and high yield agricultural
CC products, e.g. fruits, ornamentals, vegetables, cereals and field crops
CC having reduced spots, blemishes and blotches that are caused by
CC pathogens, agricultural products with increased shelf-life and reduced
CC handling costs and high quality and yield crops for agricultural
CC (e.g. cereal and field crops), industrial (e.g. oilseeds) and commercial
CC (e.g. fiber crops) purposes. The present sequence is that of Abraxidopsis
CC thaliana CDPK2 of the invention.
XX
XX Sequence 1747 BP; 516 A; 316 C; 392 G; 523 T; 0 other;
Query Match 100.0%; Score 1747; DB 24; Length 1747;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1747; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 481 GAGGCTTGTCATTCCTTGGTGTATGATAGAGATCTCAAACTGAGAAATTCCTTGTGTT 540
Qy 541 GATAGTCCTAAAGATGATGCTAAAGCTTAAAGGCTACCGATTTGGTGTGTTCTGCTCTAT 600
Db 541 GATAGTCCTAAAGATGATGCTAAAGCTTAAAGGCTACCGATTTGGTGTGTTCTGCTCTAT 600
Qy 601 ARGCCAGGACATATTTATGATGCTAGTGTGAAGTGTGCTACTATGTTGCCACAGAGGTG 660
Db 601 ARGCCAGGACATATTTATGATGCTAGTGTGAAGTGTGCTACTATGTTGCCACAGAGGTG 660
Qy 661 CTAAGAAATGTTTANGACCTCAAAATAGATGTGTGGAGTGTGTGTTTATCCTCTACATT 720
Db 661 CTAAGAAATGTTTATGACCTCAAAATAGATGTGTGGAGTGTGTGTTTATCCTCTACATT 720
Qy 721 TTACTCAGCGGTGTTCTCCCTCTCGGGCAGAGACTGAGTCTGGAATCTTTAGACAGATA 780
Db 721 TTACTCAGCGGTGTTCTCCCTCTCGGGCAGAGACTGAGTCTGGAATCTTTAGACAGATA 780
Qy 781 TTGCAAGGGAAGTTAGATTTCAAAATCTGACCCGTGGCCTACTATCTCAGAAAGCTGCTAAA 840
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Db 841 GATTTGATCTATAAATGCTCGAAGAGCCCAAGAACGACGATTTCTGCTCATGAAGCC 900
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Db 901 TTGTGTCACCCATGATTTGATGATGAACAGCAGCACCAGACGCTTTGATCCAGCA 960
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Db 1021 GTAATTCCTGAGACATTTTCAGAGGAAGAAATTTGAGGTCTCTGAAGGAATTTGTTCAAGATG 1080
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Qy 1441 ACAGCAATGATGAGGAAGGAGATGAGTTGGGAGAGCAGAACCCATGATGAAGAACTTG 1500
Db 1441 ACAGCAATGATGAGGAAGGAGATGAGTTGGGAGAGCAGAACCCATGATGAAGAACTTG 1500
Qy 1501 AACTTCAACATGCTGATGCTTTTGGAGTTGATGGTGGAATAATCTGATGACTGACTCATC 1560
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 QY 1741 GAATTC 1747
 Db 1741 GAATTC 1747

RESULT 2
 ABA06022 standard; cDNA; 1657 BP.
 XX ABA06022;
 XX
 DT 08-MAR-2002 (first entry)
 DE Arabidopsis CDPK4 encoding polynucleotide SEQ ID NO 4.
 XX Arabidopsis; CDPK2; CDPK4; calcium dependent protein kinase; oilseed;
 KW disease resistance; agricultural; pathogen; crop yield; ornamental;
 KW fungicide; bactericide; nematocide; insecticide; viricide; cereal;
 KW transgenic; plant; enzyme; gene; ss.
 OS Arabidopsis thaliana.
 XX
 FH Key Location/Qualifiers
 FT 1.1506
 FT CDS /*tag= a
 FT /product= "CDPK4"
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 PN WO200184911-A1.
 XX
 PD 15-NOV-2001.
 XX
 PF 04-MAY-2001; 2001WO-US14368.
 XX
 PR 05-MAY-2000; 2000US-201925P.
 XX
 PA (GENO) GEN HOSPITAL CORP.
 XX
 PI Sheen J;
 XX
 DR WPI; 2002-062179/08.
 DR P-PSDB; AAM48001.
 XX
 XX Producing plant having increased disease resistance, comprises
 PT regenerating plant from a non-naturally occurring plant cell
 PT over-expressing a polynucleotide encoding a calcium dependent protein
 PT kinase polypeptide
 XX
 PS Disclosure; Fig 2; 44pp; English.
 XX
 CC The invention relates to producing a plant having increased disease
 CC resistance, comprising providing a non-naturally occurring plant cell
 CC over-expressing a polynucleotide encoding a calcium dependent protein
 CC kinase (CDPK) polypeptide and regenerating a plant from the plant
 CC cell, where the CDPK polypeptide is expressed in the plant, increasing
 CC the resistance of the plant to disease as compared to a
 CC naturally-occurring plant. The method is useful for a variety of
 CC agricultural and commercial purposes including improving a plant's
 CC resistance against plant pathogens, increasing crop yields, improving
 CC crop and ornamental quality and reducing agricultural production costs.
 CC The method facilitates an effective and economical method for in-plant

CC protection against plant pathogen, reducing or minimizing the need for
 CC traditional chemical practices (e.g. application of fungicides, typically
 CC bactericides, nematocides, insecticides, or viricides) that are typically
 CC used by farmers for controlling the spread of plant pathogens and
 CC providing protection against disease causing pathogens. The method
 CC contributes to the production of high quality and high yield agricultural
 CC products, e.g. fruits, ornamentals, vegetables, cereals and field crops
 CC having reduced spots, blemishes and blotches that are caused by
 CC pathogens, agricultural products with increased shelf-life and reduced
 CC handling costs and high quality and yield crops for agricultural
 CC (e.g. cereal and field crops), industrial (e.g. oilseeds) and commercial
 CC (e.g. fiber crops) purposes. The present sequence is that of Arabidopsis
 CC thaliana CDPK4 of the invention.

XX Sequence 1657 BP; 500 A; 287 C; 384 G; 486 T; 0 other;

Query Match 58.8%; Score 1202.4; DB 24; Length 1657;
 Best Local Similarity 84.1%; Pred. No. 1.6e-262;
 Matches 1384; Conservative 0; Mismatches 251; Indels 11; Gaps 2;

QY 75 GAAGCCAAACCTAGACGCTCTCAAAACACAGATTCTACCATATCAAAACACACGATTAAAG 134
 Db 6 GAAACCAACCTAGAGACCTCAACAGCTGTTCTTCATACGAAACCAAGATTAAAG 65
 QY 135 AGATCATTACCTTTCTGGAAAAAGAGCTAGGCCAAAGGCAATTTGGAAACAACCTATCTCTG 194
 Db 66 AGATCATTACCTTTCTGGAAAAAGAGCTAGGCCAAAGGCAATTTGGAAACAACCTATCTCTG 125
 QY 195 CACAGAGAAATCAACCTCGCTAATTAGCCCTGCAATTCGATCCGAAAGCGAAAGCTCGT 254
 Db 126 TACAGAGAAATCATCATCAGCTAATTACGCTTGGAAATCAATCCCAAAAGTAACTTGT 185
 QY 255 GTGTCGCGAGGATTACGAAAGATGTATGGCGTGAGATTCAAGATCATGATCATCTCTCTGA 314
 Db 186 ATGTCGTGAAGACTACGAAGATGTATGGCGTGAGATTCAAGATCATGATCATCTCTCTGA 245
 QY 315 GCATCAAAATGTTGTAGGATCAAAAGGCACTTATGAGATTCGGTGTGTTGTCATATTGT 374
 Db 245 GCATCCTAATGTTGTAGGATCAAAAGGCACTTATGAGATTCGGTGTGTTGTTTTCATATTGT 305
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 Db 306 TATGAGGTTTCTGAAGGTGGTGAGCTTTTTCGCGGATTTGTTCTAAAGGTGTTTTTAG 365
 QY 435 TGAGCGTGAAGCTGCAAGCTTATTAAGACGATTTCTGGTGTGTTGAGGCTTGTCTATTC 494
 Db 366 TGAACGTGAAGCTGCTAAAGTTGATTAAGACTATTCTTGGTGTGTTGAGGCTTGTCTATTC 425
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 Db 426 TCTTGGTGTATGTCATAGAGATCTTAAAGCTGAGAAATTTCTTGTGATAGTCTCTAAAGA 485
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 Db 666 TCTCTCTCTTCTGGGACAGAACCCAGCTGAGGAATCTTTAGGAGATATTGCAAGGGAAGAT 725
 QY 795 AGATTTCAAATCTGACCCCGTGGCTACTATCTCAGAAGCTCTCAAGATTTTGAATCTATPA 854
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Qy	1035	ACTTTTCAGAGGAAGAAATTTGGAGGTCCTAAGGAATTTGTTCAAGATATAGACACAGACAA 1094
Db	966	ACTCTCGAGGAAGAGATTGGTGGTCTGAGGAATTTCTCAAAATGATAGATACAGACAA 1025
Qy	1095	CAGCGGAACGATTACTTTTTGAAGAGCTCAAAGCGGTTTGAAGAGAGTCGGATCTGAAC 1154
Db	1026	CAGTGAACAAATCACCTTTTGAAGAGCTTAAAGCAGGCTTAAAGAGAGTTGGATCTCAAT 1085
Qy	1155	GATGGAATCAGAAATCAAGTCTCTCATGATCGCGCTGATATCGAACACAGTGGTACAAT 1214
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Qy	1215	AGACTACCGGAAATTCCTAGACGAACCTTACATGAACAAAGATGGAGAGAGAGAGAT 1274
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Qy	1275	TCTGGTGGCTGCATTTTCGGAGCTTTCACAAAGACGAAGCGTTTATATCACCATCGATGA 1334
Db	1206	CTTGGTGGTTCGCTTTTCATCTTTGATTAAGATGGTAGCGTTTATATCACCATTCACGA 1265
Qy	1335	GCTTCAGTCAGTTGACAGAGTTTGGTCTATGTGATACACCTCTGGACACATGATCAA 1394
Db	1266	GCTTCAACAAAGCCTGACAGAGTTTGGTCTCTGTGACACTCCTCTTGATGACATGATCAA 1325
Qy	1395	GGAGATTGATCTTCACAAATCACGGGAAGATCGATTCTCGGAGTTTACAGCAATGATGAG 1454
Db	1326	AGAGATTGATCTTGATTAATGACGGGAAGATTGATTTCTCAGAGTTTACTGCTATGATGA 1385
Qy	1455	GAAAGGAGATCGAGTTTCGGGAGAGCAGAACCATGATGAAGAACTTTGAACATTCACATGC 1514
Db	1386	GAAAGGAGATGGTGTTCGGGAGAGCAGAACTATGAGAAACAACCTTGAACCTTCAATATAGC 1445
Qy	1515	TGATGCTTTTCGAGTTGATGTGTGAATAATCTGATGATCGACTCATCTTCTTCACAAATT 1574
Db	1446	TGAAGCTTTTCGAGTTTGA - GACACAAAGCAGCACTGCTAAATCTGATGATTCACCAAGT 1504
Qy	1575	TCTGTTTTTTTCTCTTAAATTCGGTTATATTTTTGAAATCTTAAATTCCTTAAGGATACAAA 1634
Db	1505	AATTAATATCATCTATACTTGGAAATTGAGAAATGAGAAGT-----CACAAAG 1554
Qy	1635	AATATATCTCGCTGTTTTTTCGTTCTCTTTTTTATTTTTTGTACATGAGCAACTTCTTAA 1694
Db	1555	AAAACATGAATCTTCCCTTTTGTGTTTTCGTTTCCACTTTTGTAGATGAGCAACTTCTCA 1614
Qy	1695	ATTTTTATCCTCATATGGATAATTTT 1720
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RESULT 3
AAC44687
ID AAC44687 standard; DNA; 1506 BP.
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XX
AC AAC44687;
XX
XX DT 18-OCT-2000 (first entry)
XX
XX DE Arabidopsis thaliana DNA fragment SEQ ID NO: 43752.
XX
XX Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.


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PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
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PR 21-JUL-1999; 99US-0145088.
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PR 22-JUL-1999; 99US-0145087.
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PR 23-JUL-1999; 99US-0145218.
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PR 27-JUL-1999; 99US-0145913.
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PR 09-AUG-1999; 99US-0147493.
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PR 13-AUG-1999; 99US-0148565.
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PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
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PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152263.
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PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
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PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
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PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
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PR 21-OCT-1999; 99US-0160814.
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PR 22-OCT-1999; 99US-0160980.
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PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
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PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

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Query Match 67.7%; Score 1183.2; DB 21; Length 1506;

Best Local Similarity 88.2%; Pred. No. 3.5e-258; Indels 0; Gaps 0;
Matches 1287; Conservative 0; Mismatches 173;

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QY 75 GAAGCCAAACCTAGAGCTCCTTCAAAACACAGTTTACCATATCAAAACACCAAGATTAAAG 134
DB 6 GAACCAAACCTAGAGACCTCAACAGTGTCTTCCATACGAAACACCAAGATTAAAG 65
QY 135 AGATCAATTACCTTCGGGAAAAAGCTAGCCCAAGGCCAATTTGGACACCTATCTCTG 194
DB 66 AGATCACTATCTCTCGGCAAAAAGCTAGCCCAAGGCCAATTTGGACCAACCTATCTCTG 135
QY 195 CACAGAGAAATCAACCTCCGCTAATTACGCTGCAATCGATCCCGAAGCGAAAGCTCGT 254
DB 126 TACAGAGAAATCAATCACTAATTTACGCTTGAATCAATCCCAAAACGTAAGCTTGT 185
QY 255 GTGTCGCGAGGATTACGAAGATGTATGGCGTGAGATTGAGATCATGATCATCTCTCTGA 314
DB 186 ATGTCGTGAAGACTACGAAGATGTATGGCGTGAGATTGAGATCATGATCATCTCTCTGA 245
QY 315 GCATCCAAATGTGTAGATCAAAAGGACCTTATGAAGATTCGGTGTCTTCTCATATTGT 374
DB 246 GCATCTAATGTGTAGAAATCAAGGCTACTTATGAAGACTCTGTTTTTGTTCACATTGT 305
QY 375 TATGAGGTTTGTGAAGCTGTGAGCTTTTGTATCGGATTTCTTAAAGGTCATTTTAG 434
DB 306 TATGGAAGTTTGTGAAGCTGTGAGCTTTTGTATCGGATTTCTTAAAGGCTGTTTGTAG 365
QY 435 TGAGCGTGAAGCTGTCAAGCTTATTAAGACGATTTCTTGGTGTCTTGTGAGGCTTGTCTATTC 494

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Db 366 TGAAGCTGAAGCTGCTAAAGTGAATTAAGACTATCTCTGGTGTGTTGAGGCTTGCTATTC 425
QY 495 TCTTGTGTTTATGATAGAGATCTCAAAACCTGAGAAATTTCTTGTGTTGATAGTCTTAAAGA 554
Db 426 TCTTGTGTTTATGATAGAGATCTTAAAGCTGAGAAATTTCTTGTGTTGATAGTCTTAAAGA 485
QY 555 TGAATGATAGCTTAAGCTTACGATCGATTTTGGTTTGTCTGCTTCTATAGCCAGGACAAATA 614
Db 486 TGAATGATAGCTTAAGCTTACGATCGATTTTGGTTTGTCTGCTTCTATAGCCAGGACAAATA 545
QY 615 TTTATATGAGCTAGTTGGAAGTCCGTACTATGTTCCACAGAGGTGCTTAAAGAAATGTTA 674
Db 546 TCTGTATGATGTTGGAAGTCCGTATATGTTCCACAGAGGTGCTTAAAGAAATGTTA 605
QY 675 TGAACCTGAAATAGATGTTGAGAGTCTGCTGCTTCTTCTATAGCCAGGACAAATA 734
Db 606 TGAACCTGAAATAGATGTTGAGAGTCTGCTGCTTCTTCTATAGCCAGGACAAATA 665
QY 735 TCTCTCCCTTCTGGGACAGACTGAGTCTGGAATCTTTAGACAGATATTTGCAAGGGAAGTT 794
Db 666 TCTCTCCCTTCTGGGACAGACTGAGTCTGGAATCTTTAGACAGATATTTGCAAGGGAAGAT 725
QY 795 AGATTTCAAAATCTGACCCGTGGCTACTATCTCAGAGCTGCTTAAAGATTTGATCTATAA 854
Db 726 AGATTTCAAAATCTGACCCGTGGCTACTATCTCAGAGCTGCTTAAAGATTTGATCTATAA 785
QY 855 AATGCTCGAAGGAGCCCAAGAAAGCCATTTCTGCTCATGAAGCCTTGTGTACCCCATG 914
Db 786 AATGCTCGAAGGAGCCCAAGAAAGCCATTTCTGCTCATGAAGCCTTGTGTACCCCATG 845
QY 915 GATTTGCTGATGACAGAGCAGACAGCAAGCCTTGTGATCCAGAGTCTTATCTCGTCT 974
Db 846 GATTTGCTGATGACAGAGCAGACAGCAAGCCTTGTGATCCAGAGTCTTATCTCGTCT 905
QY 975 AAAGCAGTCTTCTCAAAATGAATGAATTAAGAAATGCGATTAACGGTAAATCTCTGAGAG 1034
Db 906 TAAGCAGTCTTCTCAAAATGAATGAATTAAGAAATGCGATTAACGGTAAATCTCTGAGAG 965
QY 1035 ACTTTGAGAGAAATGGAAGTCTGAAGGAATTTGTTCAAGATGATAGACAGACAA 1094
Db 966 ACTCTCGAGAGAGAGATGCTGCTGCTGAAGGAATTTGTTCAAAATGATAGATAGACAA 1025
QY 1095 CAGCGGACGATTAATTTGAGAGCTCAAGCGGTTTGAAGAGAGTGGATCTGAACT 1154
Db 1026 CAGTGGAAATCACTTTGAGAGCTTAAAGAGCTTAAAGAGAGTGGATCTGAACT 1085
QY 1155 GATGGAATCAGAAATCAAGTCTCTCATGATGCGGCTGATATCGACAAAGTGTACAAAT 1214
Db 1086 GATGGAATCAGAAATCAAGTCTCTCATGATGCGGCTGATATCGACAAAGTGTACAAAT 1145
QY 1215 AGACTACGAGAGTCTTACGAGCAACCTTACATGAAACAGATGAGAGAGAGAT 1274
Db 1146 AGACTACGAGAGTCTTACGAGCAACCTTACATGAAACAGATGAGAGAGAGAT 1205
QY 1275 TGTGTGCTGCTGATTTTGGGCTTTGATGATGATGATGATGATGATGATGATGATGATGAT 1334
Db 1206 CTGTGTGCTGCTGATTTTGGGCTTTGATGATGATGATGATGATGATGATGATGATGATGAT 1265
QY 1335 GCTTCAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1394
Db 1266 GCTTCAACAGCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1325
QY 1395 GGAGAT 1454
Db 1326 AGAGAT 1385
QY 1455 GAAAGAGAT 1514
Db 1386 GAAAGAGAT 1445
QY 1515 TGATGCTTTTGGAGTTGATG 1534

Db 1446 TGAAGCTTTTGGAGTTGAGG 1465
RESULT 4
AAF74274
ID AAF74274 standard; DNA; 1768 BP.
XX
AC AAF74274;
XX
DT 04-MAY-2001 (first entry)
XX
DE Soybean calcium dependent protein kinase clone #2.
XX
KW Calcium dependent protein kinase; CDPK; herbicide resistance;
KW paraquat; diquat; crop production; ds.
XX
OS Glycine max.
XX
PN WO200107592-A2.
XX
PD 01-FEB-2001.
XX
PF 26-JUL-2000; 2000WO-GB02876.
XX
PR 27-JUL-1999; 99GB-0017642.
XX
PA (ZENE) ZENECA LTD.
XX
PI Holt CD, White AJ, Michael AJ, Osborn RW;
XX
DR WPI; 2001-168549/17.
XX
PT Producing herbicide resistance plants by inhibiting calcium dependent
PT protein kinase in plants or by providing an intracellular vacuolar
PT transporter capable of transporting agrochemical into plant vacuole
XX
PS Claim 18; Page 37; 50pp; English.
XX
CC The present invention describes a method of producing plants which are
CC resistant to the herbicides paraquat and diquat, involving inhibiting in
CC the plants a calcium dependent protein kinase (CDPK) and selecting those
CC plants which are resistant to the agrochemical of interest. This is
CC useful in the production of crops with herbicide resistance.
XX
SQ Sequence 1768 BP; 511 A; 325 C; 464 G; 468 T; 0 other;
Query Match 43.3%; Score 756.4; DB 22; Length 1768;
Best Local Similarity 70.6%; Pred. No. 1.6e-161;
Matches 1009; Conservative 0; Mismatches 421; Indels 0; Gaps 0;
QY 106 GTTCTACCATATCAAAACACACAGATTAAGAGATCATACCTCTCGGAAAGGCTAGGC 165
Db 195 GTTCTCCCGCAGCGCACGAGACATCCGTGAGGTGACGAGTTGGGCGGAGCTCGG 254
QY 166 CAAGGCCAATTTGGAACACACCTATCTCTGCACAGAGAAATCAACCTCCGCTAATTTACGCC 225
Db 255 CAGGGCCCAATTCGGGACCCCTTCGAGTGCACGGCGCGTGCAGTGGTGGGAAGTTCCGC 314
QY 226 TGCAATTCGATCCCGAAGCAAGCTGCTGTGTCGCGAGGATTAAGAGATGATGCGGT 285
Db 315 TGCAAGTGCATTCGGAAGCGGAAGCTGCTGTGCAAGGAGGACTACGAGACGTGTGGCG 374
QY 286 GAGATTCAGATCATGATCATCTCTCTGAGCATCCAAATGTTGTTAGGATCAAGGGACT 345
Db 375 GAGATTCAGATTAATGCACCACTTGTTCGGAACACGCCAAGCTTGTCCGATCGAAGGAGC 434
QY 346 TATGAAGATTCGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 405
Db 435 TACGAGGATTCACCGCGCTGCACCTGGTCAATGAGTGTGCGAGGTTGAGAGTTGTT 494
QY 406 GATCGGATTTCTTAAAGCTCAATTTAGTACGCGTGAAGCTGTCAAGCTTATTAAAGAGC 465
Db 495 GACAGGATTCGTGCAAGAGGAGACACTACAGCAGAGACAGCGCGGAGGTTGATTAAGAGC 554

2Y 466 ATTCTGTGTTGTGAGGCTTGTCATTCTCTTGGTGTATGTCATAGAGATCTCAAACT 525
 Db 555 ATTGTGAGGTTGTTAGCGGTGTCACCTGCTAGGGGTGTCATAGGACCTTAAGCCT 614
 2Y 526 GAGATTTCTTGTGTAGTGTCTTAAGAGTATGCTTAAGCTTAAGGCTACCGATTTTGGT 585
 Db 615 GAGATTTCTTGTGTAGTGTCTTAAGAGTATGCTTAAGCTTAAGGCTACCGATTTGCGC 674
 2Y 586 TTGCTGTCTTCTTATAAGCCAGGCAATATTTATATGACGTAGTGAAGTCCGTACTAT 645
 Db 675 TTGCTGTCTTCTTATAAGCCAGGCAATATTTATATGACGTAGTGAAGTCCGTACTAT 734
 2Y 646 GTTGACACAGAGTCTTAAGAAATGTTATGACCTGAAATAGATGTTGAGTGTCTGGT 705
 Db 735 GTTGACACAGAGTCTTAAGAAATGTTATGACCTGAAATAGATGTTGAGTGTCTGGG 794
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 Db 795 GTTATCTCTTACATTTTACTCAGCGGTGTTCTCTCCCTTCTGGGCGGCAATCTGAACCGGG 854
 2Y 766 ATCTTTAGACAGATATTCAGAGGAGTTAGATTTCAATCTGACCGTGGCTTACTATC 825
 Db 855 ATCTTTCCGACAGATTTTACTAGGAAATCTGATTTTCAATCTGACCGTGGCTTACTATC 914
 2Y 826 TCAGAGCTGCTTAAGATTTGATCTATAAATGCTTCGAAAGGAGCCCAAGAAACGCATT 885
 Db 915 TCAGAGCTGCTTAAGATTTGATCTATAAATGCTTCGAAAGGAGCCCAAGAAACGCATT 974
 2Y 886 TTGCTCATGAAGCCTTGTGTCACCCATGATTTGTCGATGAACAGAGCAGCAGAGCAAG 945
 Db 975 ACAGACATGAAGTCTCGCCACCCATGATTTGTCGATGAACAGAGCAGCAGAGCAAG 1034
 2Y 946 CCTCTGATCCAGAGTCTTATCTGCTTAAGAGAGTTTCTCAAAATGAATGAATTAAG 1005
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 2Y 1246 CACATGAACAGATGGAGAGAGAGATTTCTGGTGTGATTTTGGACTTTGACAAA 1305
 Db 1335 CATTAAATGAGCTGGAGAGAGAGAAACCTAGTGTGGCTTCTCTATTTTGACAAA 1394
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 Db 1455 GATGATATCAATTTGACGACATGATCAAGGAAATTTGATCAAGATAACGATGGCAATA 1514
 2Y 1426 GATTTCTCGAGTTTACAGCAATGATGAGAAAGGAGATTTGGGAGAGAGCAAC 1485
 Db 1515 GATTTCTCGAGTTTACAGCAATGATGAGAAAGGAGATTTGGGAGAGAGCAAC 1574
 2Y 1486 ATGATGAGAGTGTGATCTCAATTTGATGCTTTTGGAGTTGATGG 1535
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RESULT 5
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 ID AAC42924 standard; DNA; 1671 BP.
 XX
 AC AAC42924;
 XX
 DT 17-OCT-2000 (first entry)
 XX
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 37370.
 XX
 KW Hybridisation assay; genetic mapping; gene expression control;
 KW protein identification; signal transduction pathway;
 KW metabolic pathway; promoter; termination sequence; ss.
 XX
 OS Arabidopsis thaliana.
 XX
 FN EP1033405-A2.
 XX
 PD 06-SEP-2000.
 XX
 PF 25-FEB-2000; 2000EP-0301439.
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 PR 28-OCT-1999; 99US-0161992.
 PR 28-OCT-1999; 99US-0161993.
 PR 29-OCT-1999; 99US-0162142.

Query Match 39.4%; Score 688.4; DB 21; Length 1671;
 Best Local Similarity 67.2%; Pred. No. 3.8e-146;

Matches 974; Conservative 0; Mismatches 476; Indels 0; Gaps 0;

QY 73 ACAGAGCCAAACCTTAGCGTCTTCAACACAGTTCATATCAACACACGATTA 132
 Db 220 ATGAGGCGTAACCCAGACAACTACTATGTTTGTGTCATAAGACACCAACATT 279
 QY 133 AGAGATCATTCCTTCTGGAAAAAGGTAGCCAGGCCAAATTTGGAACAACTATCTC 192
 Db 280 CGTGATATCTATACCTTAGCCGCGAGCTAGGTCAAGTCAATTTGGACGACTTACTA 339
 QY 193 TGCACAGAGAATCAACCTTCGCTAATTAGCCTGCAAAATCGATCCGACGGAAGCTC 252
 Db 340 TGTACAGAGATTGCTTCAGGCGGTTGACTACGCTTGTAAAGTCAATATCCAGAGGAGTTG 399

QY	1333	GAGCTTCAGTCAGCTTGACAGAGTGTGGTCTATGTGATACACCTCTGGACGACATGATC	1339			
Db	1480	GAGCTACACAAAGCGTGTGTTGAACATGGCATGGCTGATGTTTTCTTGAAGACATCATC	1539			
QY	1393	AAGGAGATTGATCTTTGACAAATGACGGGAAGATCGATTCTCGGAGTTTACAGCAATGATG	1452			
Db	1540	AAAGAGTTGATCAAAAACAATGATGGAAGATTGATTATGGTGAAGTTGTGGAGATGATG	1599			
QY	1453	AGGAAAGGAGATGGAGTTGGGGAAGACGAGAACCAATGATGAAGAACTTGAACATTCACAACTT	1512			
Db	1600	CAAAAGGGAATGCTGCTGTTGTTGAAGAGGACGATGAGAAATAGCTTAAACATTAGCATG	1659			
QY	1513	GCTGATGCTT 1522				
Db	1660	AGAGACGCT 1669				
RESULT 6						
AAF74283						
ID	AAF74283 standard; DNA; 2550 BP.					
XX	AAF74283;					
XX	04-MAY-2001 (first entry)					
XX	Cucurbita pepo calcium dependent protein kinase clone.					
DE						
DE						
XX						
KW	Calcium dependent protein kinase; CDPK; herbicide resistance;					
KW	paraquat; diquat; crop production; ds.					
XX						
OS	Cucurbita pepo.					
XX						
PN	WO200107592-A2.					
XX						
PD	01-FEB-2001.					
XX						
XX	26-JUL-2000; 2000WO-GB02876.					
XX						
PR	27-JUL-1999; 99GB-0017642.					
XX						
XX	(ZENE) ZENECA LTD.					
PA						
XX						
PI	Holt CD, White AJ, Michael AJ, Osborn RW;					
XX						
DR	WPI; 2001-168549/17.					
XX						
PT	Producing herbicide resistance plants by inhibiting calcium dependent					
PT	protein kinase in plants or by providing an intracellular vacuolar					
PT	transporter capable of transporting agrochemical into plant vacuole					
XX						
XX	Claim 18; Page 43; 50pp; English.					
XX						
CC	The present invention describes a method of producing plants which are					
CC	resistant to the herbicides paraquat and diquat, involving inhibiting					
CC	the plants a calcium dependent protein kinase (CDPK) and selecting the					
CC	plants which are resistant to the agrochemical of interest. This is					
CC	useful in the production of crops with herbicide resistance.					
XX						
XX	Sequence 2550 BP; 710 A; 467 C; 627 G; 746 T; 0 other;					
QY	Query Match 37.4%; Score 652.6; DB 22; Length 2550;					
Best Local Similarity 66.6%; Pred. No. 5.5e-138;						
Matches 934; Conservative 0; Mismatches 469; Indels 0; Gaps						
QY	67	ATGGAGACGAAGCCAAACCCCTAGAGCTCTCTCAAAACACAGTTCTACCATATCAAAACCA	126			
Db	843	ATGAGAGGGTGGGTAGTGTGGCTTCGAGTGGTTCGGTTCTACACAGAAAACGGGA	902			
QY	127	CGATTAGAGATCATTTACCTTCGGGMAAAAAGCTAGGCCAAGGCCAATTTGGACACACC	186			
Db	903	AACTTTAAGGAGTAATTATAGCTTGGGTAAAAAATTAGGCCAAGGCAATTTGGGACACA	962			
QY	187	TATCTCTGCACAGAGAAATCAACCTCCGCTTAATTAGCGCTGCAAATCGATCCGGAAGGA	246			

Db 963 TATATGTGTGGAGAGCAACTGGGAAAGATGTTGTTAAAGTCTATTGTCAGAGAGG 1022
 QY 247 AAGCTCTGTGTGGAGAGCAACTGGGAAAGATGTTGTTAAAGTCTATTGTCAGAGAGG 1022
 Db 1023 AAGTGTGTTAAAGAGAGATGTTGTTAAAGTCTATTGTCAGAGAGG 1082
 QY 307 CTCTCTGAGCATCCAAATCTGTTAGGATCAAGGAGCTTATGAAGATTCGGTGTGTT 366
 Db 1083 TTGTCTGGACACCCGAAATGTTATTCGATCAAGGGGGGTACGAGGATGCGGTGCAAT 1142
 QY 367 CATATTGTTATGAGGATGTTGTTAAAGTGTGAGCTTTTGTATCGGATGTTTCTAAAGG 426
 Db 1143 CAGGTAGTCATGAGGATGTTGTTGAGGATGAGCTTATTTGATAGGATCAATCAAGCTGGA 1202
 QY 427 CATTTAGTGAAGCTGAAGCTGTTAAAGCTTATTAAGAGATTCCTTGTGTTGTTGAGGCT 486
 Db 1203 CATTTAGTGAAGCTGAAGCTGTTAAAGCTTATTAAGAGATTCCTTGTGTTGTTGAGGCT 486
 QY 487 TGTCTATCTGTTGTTGTTATGATGATGATCTCAAACTGAGAAATTTCTTGTGTTGATGAT 546
 Db 1263 TGTCAAGCTTGTGTTGTTATGATGATGATCTCAAACTGAGAAATTTCTTGTGTTGATGAT 546
 QY 547 CCTAAAGATGATCTAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAG 606
 Db 1323 AAGGAGAGGATCACTTCTCAAGCAATGATTTTGAATCAATGATTTTGAATCAATGATTT 1382
 QY 607 GGACATATTATATGATGATGTTGAGGATGCTGATGATGTTGAGGATGCTGATGATGAT 666
 Db 1383 GGCGAAAGATTTAATGATGTTGTTGAGGATGCTGATGATGTTGAGGATGCTGATGATGAT 666
 QY 667 AATGTTATGAGCTCAAAATGATGTTGAGGATGCTGATGATGTTGAGGATGCTGATGATGAT 726
 Db 1443 AAGGATATGTTGTTGAGGATGCTGATGATGTTGAGGATGCTGATGATGTTGAGGATGCT 1502
 QY 727 AGCGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 786
 Db 1503 AGTGGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 786
 QY 787 GGGAGTTAGATTTCAAACTGAGGATGCTGATGATGTTGAGGATGCTGATGATGTTGAGGAT 846
 Db 1563 GGGAGTTAGATTTCAAACTGAGGATGCTGATGATGTTGAGGATGCTGATGATGTTGAGGAT 846
 QY 847 ATCTATAAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 906
 Db 1623 GTTAGAGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 906
 QY 907 CAGCATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 966
 Db 1683 CAGCATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 966
 QY 967 TCTGCTTAAGCAGTTTCTCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1026
 Db 1743 ACTGCTTGAAGCAGTTTCTCAATGATGATGATGATGATGATGATGATGATGATGATGAT 1802
 QY 1027 GCTGAGAGATTTTCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1086
 Db 1803 GCTGAGAGATTTTCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1086
 QY 1087 ACAGACAGAGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1146
 Db 1863 ACTGACAGAGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1222
 QY 1147 TCTGAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1206
 Db 1923 GCTAACTTAAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1266
 QY 1207 GGTACATAGACTACGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1266
 Db 1983 GGAACATGACTACGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2042
 QY 1267 GAGGAGATCTGTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1326

Db 2043 GAAGATCATCTTCTAGCAGCGTTTTCATATTTTCGACAAAGATGGAAGCGGTTTCATTACC 2102
 QY 1327 ATCGATGAGCTTCTAGCAGCGTTTTCATATTTTCGACAAAGATGGAAGCGGTTTCATTACC 2102
 Db 2103 CACGACGAGCTTCAACAAGCATGTAAGAGTTTCGGGATAGAGGATCTTCAAAATGGAAGAA 2162
 QY 1387 ATGATCAAGGAGATGATCTTTCGACAAATGACGGAAGATGCGATTTCTCGGAGTTTACAGCA 1446
 Db 2163 ATGATCGGAGGTCGATCAAAACATGACGGAAGATGCGATTTCTCGGAGTTTACAGCA 1446
 QY 1447 ATGATGAGGAAAGGAGATGAGT 1469
 Db 2223 ATGATGCAAAAGGAAATGATG 2245
 RESULT 7
 AAF74285
 ID AAF74285 standard; DNA; 2022 BP.
 XX AAF74285;
 XX AC
 XX XX
 DT 04-MAY-2001 (first entry)
 XX Vigna radiata calcium dependent protein kinase clone.
 DE Vigna radiata calcium dependent protein kinase; CDPK; herbicide resistance;
 KW Calcium dependent protein kinase; CDPK; herbicide resistance;
 KW paraquat; diquat; crop production; db.
 XX Vigna radiata.
 OS
 XX
 PN WO200107592-A2.
 XX
 PD 01-FEB-2001.
 XX
 XX 26-JUL-2000; 2000WO-CB02876.
 XX 27-JUL-1999; 99GB-0017642.
 PR (ZENE) ZENESCA LTD.
 PA
 XX Holt CD, White AJ, Michael AJ, Osborn RW;
 XX WPI; 2001-168549/17.
 DR
 XX Producing herbicide resistance plants by inhibiting calcium dependent
 PT protein kinase in plants or by providing an intracellular vacuolar
 PT transporter capable of transporting agrochemical into plant vacuole
 XX
 PS Claim 18; Page 44-45; 50pp; English.
 CC The present invention describes a method of producing plants which are
 CC resistant to the herbicides paraquat and diquat, involving inhibiting in
 CC the plants a calcium dependent protein kinase (CDPK) and selecting those
 CC plants which are resistant to the agrochemical of interest. This is
 CC useful in the production of crops with herbicide resistance.
 XX
 SQ Sequence 2022 BP; 587 A; 374 C; 466 G; 595 T; 0 other;
 Query Match 36.1%; Score 629.8; DB 22; Length 2022;
 Best Local Similarity 65.3%; Pred. No. 7.5e-133;
 Matches 925; Conservative 0; Mismatches 492; Indels 0; Gaps 0;
 QY 116 ATCAACACACGATTAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 175
 Db 140 ATAAAGCTCCCAACATTCGTGATCTATACATCTTGGCGCAATTTGGACAGGACAAT 199
 QY 176 TTGGAACAACCTTCTCGACAGAGAAATCAACCTCGCTAAATAGCCTGCAATCGA 235
 Db 200 TTGCACCATTTTATGACCGGAGATTTCTCTTCAATGATATGCTTGCATATCTA 259
 QY 236 TCCGAGCGAAAGCTGTTGTTGCGGAGGATTTACGAAGATGTTGCGGTGAGATTGAGA 295
 Db 260 TCTCCAAAGAAAGTTGATTTCCAAAGGAGGATGTTGAGGATGTCAGGAGGAAATTCAGA 319

PR 07-JUN-1999; 99US-0137724.
 PR 08-JUN-1999; 99US-0138094.
 PR 10-JUN-1999; 99US-0138540.
 PR 10-JUN-1999; 99US-0138847.
 PR 14-JUN-1999; 99US-0139119.
 PR 16-JUN-1999; 99US-0139452.
 PR 16-JUN-1999; 99US-0139453.
 PR 17-JUN-1999; 99US-0139492.
 PR 18-JUN-1999; 99US-0139454.
 PR 18-JUN-1999; 99US-0139455.
 PR 18-JUN-1999; 99US-0139456.
 PR 18-JUN-1999; 99US-0139457.
 PR 18-JUN-1999; 99US-0139458.
 PR 18-JUN-1999; 99US-0139459.
 PR 18-JUN-1999; 99US-0139460.
 PR 18-JUN-1999; 99US-0139461.
 PR 18-JUN-1999; 99US-0139462.
 PR 18-JUN-1999; 99US-0139463.
 PR 18-JUN-1999; 99US-0139750.
 PR 18-JUN-1999; 99US-0139763.
 PR 21-JUN-1999; 99US-0139817.
 PR 22-JUN-1999; 99US-0139899.
 PR 23-JUN-1999; 99US-0140353.
 PR 23-JUN-1999; 99US-0140354.
 PR 24-JUN-1999; 99US-0140695.
 PR 28-JUN-1999; 99US-0140823.
 PR 28-JUN-1999; 99US-0140931.
 PR 30-JUN-1999; 99US-0141287.
 PR 01-JUL-1999; 99US-0141842.
 PR 01-JUL-1999; 99US-0142154.
 PR 02-JUL-1999; 99US-0142055.
 PR 06-JUL-1999; 99US-0142390.
 PR 08-JUL-1999; 99US-0142803.
 PR 09-JUL-1999; 99US-0143920.
 PR 12-JUL-1999; 99US-0143977.
 PR 13-JUL-1999; 99US-0143542.
 PR 14-JUL-1999; 99US-0143624.
 PR 15-JUL-1999; 99US-0144005.
 PR 16-JUL-1999; 99US-0144085.
 PR 16-JUL-1999; 99US-0144086.
 PR 19-JUL-1999; 99US-0144325.
 PR 19-JUL-1999; 99US-0144331.
 PR 19-JUL-1999; 99US-0144332.
 PR 19-JUL-1999; 99US-0144333.
 PR 19-JUL-1999; 99US-0144334.
 PR 19-JUL-1999; 99US-0144335.
 PR 20-JUL-1999; 99US-0144352.
 PR 20-JUL-1999; 99US-0144632.
 PR 20-JUL-1999; 99US-0144684.
 PR 21-JUL-1999; 99US-0144814.
 PR 21-JUL-1999; 99US-0145086.
 PR 21-JUL-1999; 99US-0145088.
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 PR 22-JUL-1999; 99US-0145089.
 PR 22-JUL-1999; 99US-0145192.
 PR 23-JUL-1999; 99US-0145145.
 PR 23-JUL-1999; 99US-0145218.
 PR 23-JUL-1999; 99US-0145224.
 PR 26-JUL-1999; 99US-0145276.
 PR 27-JUL-1999; 99US-0145913.
 PR 27-JUL-1999; 99US-0145918.
 PR 27-JUL-1999; 99US-0145919.
 PR 28-JUL-1999; 99US-0145951.
 PR 02-AUG-1999; 99US-0146386.
 PR 02-AUG-1999; 99US-0146388.
 PR 02-AUG-1999; 99US-0146389.
 PR 03-AUG-1999; 99US-0147038.
 PR 04-AUG-1999; 99US-0147204.
 PR 04-AUG-1999; 99US-0147302.
 PR 05-AUG-1999; 99US-0147192.
 PR 05-AUG-1999; 99US-0147260.
 PR 06-AUG-1999; 99US-0147303.

PR 06-AUG-1999; 99US-0147416.
 PR 09-AUG-1999; 99US-0147493.
 PR 09-AUG-1999; 99US-0147935.
 PR 10-AUG-1999; 99US-0148171.
 PR 11-AUG-1999; 99US-0148319.
 PR 12-AUG-1999; 99US-0148341.
 PR 13-AUG-1999; 99US-0148565.
 PR 13-AUG-1999; 99US-0148684.
 PR 16-AUG-1999; 99US-0149368.
 PR 16-AUG-1999; 99US-0149369.
 PR 18-AUG-1999; 99US-0149175.
 PR 18-AUG-1999; 99US-0149426.
 PR 20-AUG-1999; 99US-0149722.
 PR 20-AUG-1999; 99US-0149723.
 PR 20-AUG-1999; 99US-0149929.
 PR 23-AUG-1999; 99US-0149902.
 PR 23-AUG-1999; 99US-0149930.
 PR 25-AUG-1999; 99US-0150566.
 PR 26-AUG-1999; 99US-0150884.
 PR 26-AUG-1999; 99US-0151065.
 PR 27-AUG-1999; 99US-0151066.
 PR 27-AUG-1999; 99US-0151080.
 PR 30-AUG-1999; 99US-0151303.
 PR 31-AUG-1999; 99US-0151438.
 PR 01-SEP-1999; 99US-0151930.
 PR 07-SEP-1999; 99US-0152363.
 PR 10-SEP-1999; 99US-0153070.
 PR 13-SEP-1999; 99US-0153758.
 PR 15-SEP-1999; 99US-0154018.
 PR 16-SEP-1999; 99US-0154039.
 PR 20-SEP-1999; 99US-0154779.
 PR 22-SEP-1999; 99US-0155139.
 PR 23-SEP-1999; 99US-0155486.
 PR 24-SEP-1999; 99US-0155659.
 PR 28-SEP-1999; 99US-0156458.
 PR 29-SEP-1999; 99US-0156596.
 PR 04-OCT-1999; 99US-0157117.
 PR 05-OCT-1999; 99US-0157753.
 PR 06-OCT-1999; 99US-0157865.
 PR 07-OCT-1999; 99US-0158029.
 PR 08-OCT-1999; 99US-0158232.
 PR 12-OCT-1999; 99US-0158369.
 PR 13-OCT-1999; 99US-0159293.
 PR 13-OCT-1999; 99US-0159294.
 PR 14-OCT-1999; 99US-0159329.
 PR 14-OCT-1999; 99US-0159330.
 PR 14-OCT-1999; 99US-0159331.
 PR 14-OCT-1999; 99US-0159637.
 PR 14-OCT-1999; 99US-0159638.
 PR 18-OCT-1999; 99US-0159584.
 PR 21-OCT-1999; 99US-0160741.
 PR 21-OCT-1999; 99US-0160767.
 PR 21-OCT-1999; 99US-0160768.
 PR 21-OCT-1999; 99US-0160770.
 PR 21-OCT-1999; 99US-0160814.
 PR 21-OCT-1999; 99US-0160815.
 PR 22-OCT-1999; 99US-0160980.
 PR 22-OCT-1999; 99US-0160981.
 PR 22-OCT-1999; 99US-0160989.
 PR 25-OCT-1999; 99US-0161404.
 PR 25-OCT-1999; 99US-0161405.
 PR 26-OCT-1999; 99US-0161359.
 PR 26-OCT-1999; 99US-0161360.
 PR 26-OCT-1999; 99US-0161361.
 PR 28-OCT-1999; 99US-0161920.
 PR 28-OCT-1999; 99US-0161922.
 PR 28-OCT-1999; 99US-0161933.
 PR 29-OCT-1999; 99US-0162142.

Query Match 34.2%; Score 597.4; DB 21; Length 3054;
 Best Local Similarity 63.6%; Pred. No. 1.8e-125;
 Matches 947; Conservative 0; Mismatches 506; Indels 36; Gaps 1;

1107	QY	TACTTTTGAAGAGCTCAAAAGCGGGTTTGAAGAGAGAGTCCGGATCTCTGAACCTGATGGNAATCAGA	11166
2634	Db	CACTTTTCGAAGAACTGAAAGAGCAGGACTAAAAACGAGTTTGGTGCCAAATCTCAAAGAGTCCAGA	26933
1167	QY	AATCAAGTCTCTCATGAGATCGGGCTGATATCGACAACAGTGGTACAAATAGACTACGAGAGA	12226
2694	Db	GATTCTTGATCTAAATGCGAAGCTGCTGATGTGACACANTAGCGGAACGATAGACTACAAAGA	27533
1227	QY	ATTCTTAGCAGCAACCTTACACATGAACAAGATGCGAGAGAGAGAGATTCTTGGTGGCTGC	12866
2754	Db	GTTATAGCCGCCACATTGTCATCTAAACAAAATAGAGAGAGAGACCATTGTTTCGCCGC	28133
1287	QY	ATTTTCGGACTTTTGACAAAGACGGAGCGGTTTATATACCATCGATGAGCTTCAGTCAAGC	13466
2814	Db	CTTCTCTTACTTTGACAAAGACGAGAGTGGCTTTTATCACCCCGACGAGCTTCAACAAGC	28773
1347	QY	TTGCACAGAGTTTGGTCTATGTGATACACCTCTGGACGACATGATCAAGGAGATTGTATCT	14066
2874	Db	TTGCGAAGAGTTTGGTGTGTGAAGATGCCCGCATAGAGAAATGATCGCGATGTTGATCA	29333
1407	QY	TGACAATACGGGAAGATCGATTCTTCGGAGTTTACAGCAATGATGAGGAAGAGAGATGG	14666
2934	Db	AGCAAGGATGACGNATAGACTACAAACGAGTTTCTGGCANTGATGAGAAAGGAGCAT	29933
1467	QY	AGTTGGGGAAGCAAGAACCATGATGAAGAACTTGAACTTCAACATTGCT	15153
2994	Db	AATGGGAGGACCTGTGAAGATCGGTTTATAGAGAACAGCATTTAGCATTTCT	30423

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ID AAF74277 standard: DNA: 2334 BP.

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KW paraquat:

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Best Local Similarity 62.2%; Pred. No. 1.3e-119; Matches 899; Conservative 0; Mismatches 546; Indels 0; Gaps 0;

Qy 91 CGTCTTCAACACAGTTTACCATATCAACACACAGATTAAAGATCATTTACCTTCTG 150
Db 531 CCTACATCTATCAATGTCTTGGCGGAGACACAGCGAGCCTAAGGAGCATTTATATCAT 590

Qy 151 GGAATAAGCTAGCCAAAGCCAAATTTGGAAACACTATCTCTGCACAGAGAAATCAACC 210
Db 591 GGTGGAGCTTGTTCAGGCCAGTTTGGGACAACTTACCTCTGTACCGAGATCAATACA 650

Qy 211 TCCGCTAATACGCTCAATCGATCCGAAAGCGAAAGCTGTGTGTGCGGAGATTTAC 270
Db 651 GGGTGTGATGTCTTCAAGACCATCCCAAGCGCAAGCTCATCAACCAAGGAGATGTA 710

Qy 271 GAAGATGTATGGGTGAGATTCAGATCATCATCATCTCTCTGAGCATCAAAATGTGTT 330
Db 711 GAAGATGTGCGCGGTGAGATTCAGATCAATGACCATTTGTGCGGCCAAGAATGTGTT 770

Qy 331 AGGATCAAGGAGCTTATGAAGATTCGGTGTGTTGTTTCATATTTGTTGAGGTTTGTGAA 390
Db 771 GCAATCAGAGATGCTATGAGATGGGCAAGCGGTGCACATTTGTGATGAGCTCTCGCT 830

Qy 391 GGTGTGAGCTTTTGTATCGGATTTGTTCTAAGGTCAATTTAGTGAGCGTGAAGCTGTC 450
Db 831 GGTGGGAGCTTTTGTACAGGATTCAGGAGAAGGGGATTCACGCGAGCGGAAGGCTGCA 890

Qy 451 AAGCTTATTAAGACGATTTCTTGGTGTGTTGTTGAGGCTTGTCAATCTCTGTGTGTTATGCA 510
Db 891 GAGCTTATAAGATTAATTTGTGAGCATTTGTGCTATGTGCCATTCGCTCGGGGTGATGCA 950

Qy 511 AGAGATCTAAACCTGAGATTTCTTGTGTTGATAGTCTTAAGATGATGTAAGCTTAAG 570
Db 951 CGTGTCTTAAAGGAGAAATTTCTCTCTTTTGGATAAGATGATGATCTGTCAATAAG 1010

Qy 571 GCTACGATTTTGTGTTCTCTTCTATAGCCAGGACAAATTTATATGAGCTAGTT 630
Db 1011 GCAATAGATTTTGTGTTCTATCGGTGTTCTTCAACAGGTCAAGTTTTCAGTGAAGCTGTT 1070

Qy 631 GGAAGTCCCTATATGTTGCAACAGAGTGTGTAAGAAATGTTATGACCTGAATAGAT 690
Db 1071 GGGAGTCCATATATTTGCTCTCTGAGTATTTGCAAAACGTTATGGACCAAGATCTGAT 1130

Qy 691 GTGTGGAGTGTGGTGTATCTCTACATTTTACTCAGCGGTGTCTCTCTCTCTGCGCA 750
Db 1131 GTGTGTGAGTGTGAGTATCTTACGTTTGTGCTGAGTGTGAGTGTGAGTGTGAGTGTG 1190

Qy 751 GAGACTGAGTGTGGAATCTTTAGACAGATATTTGCAAGGAGTGTGATTTCAATCTGAC 810
Db 1191 GAGACACACACAGGAATATTTGATGAGTCTTGAAGGCTGCAATTTTCAATCTGAT 1250

Qy 811 CCGTGGCTTACTTCTCAGAGCTGCTAAGATTTGATCTATAAAATGCTGAAAGGAGC 870
Db 1251 CCATGGCCAAAGATATCTGACAGTCAAAAGGATCTTATTAAGAAATGCTCTCTCATTCG 1310

Qy 871 CCCAAGAAAGCAGCTTTCTGCTCATAGGCTTTGTGTACCCATGGAATGTGATGAAACA 930
Db 1311 CCTTCGAGCGTTTGAAGGCCCATGAAGTGTCTGAAGCATCTTGGATCTGTGAAATGGA 1370

Qy 931 GCAGACACACAGAGCTTGTGATCAGAGCTTATCTCTGCTAAGCAGTTTCTCAA 990
Db 1371 GTTCCCACTGATCAGCTCTGAGTCCGAGTGTATCTCTCGGCTCAACAAATCTCTGCA 1430

Qy 991 ATGAATAAGATTAAGAAATGCGATTTACGGGTAAATGCTGAGAGCTTTTCAGAGAGAA 1050
Db 1431 ATGACAAAGTAAAGAGTTTGGCTGAGAGTGTAGTGTGAGCTCTTTCAGAGAGGAG 1490

Qy 1051 ATTGAGGTCTGAAGGAATTTGTTCAAGATGATAGACACACAGCGGAGGAGCTTACT 1110
Db 1491 ATTGCTGGTTTAAAGAAATGTTTCAAGCGAGTGTGACACAAAAATAGAGGTGTATCAT 1550

Qy 1111 TTTGAAGAGCTCAAGCGGGTTTGAAGAGAGTGGATCTGAACTGATGAATCAGAAATC 1170

Db 1551 TTGGTGAAGCTTTAGAGAAAGTTTAAAGAGATTTGGCGCTGAATTTAAGGATACAGAGATT 1610

Qy 1171 AAGTCTCTCATGATCGCGCTGATATCGACAAACAGTGTGTACAAATAGACTACGGGAATTC 1230

Db 1611 GGTGATATTAATGGAAGCGGCACACAAACGACAATAATGTAAACAATCCATTATGAAGAATTT 1670

Qy 1231 CTAGAGCAACCTTACACATGAACAAGATGGAGAGAGAGATTCTGTGGCTGCAATTT 1290

Db 1671 ATTGCTGCAACTCTACCTCTTAAACAAGATAGAAACGTGAGGAGCACCTCTGGCAGCTTTT 1730

Qy 1291 TCGGACTTTTGAACAAAGACGGAAGCGGTTATATCAACATCGATGAGCTTTCAGTCAAGCTTTC 1350

Db 1731 ACATATTTTGACAAAGATGGAGTGTGTTATATCAAGTTGACAGCTTCAACGAGCTTGT 1790

Qy 1351 ACAGAGTTTGGTCTATGTGATACACCTCTGGACGACATGATCAAGGAGATGATCTTGAC 1410

Db 1791 GGAGAACATAACATGAGGAGTTCACTCTTGAAGAGATTAITTTCAAGAGTTGATCAAAAC 1850

Qy 1411 AATGACGGGAGATTCGATTTCTCGGAGTTTACAGCAATGATGAGGAAAGGAGATGGAGTT 1470

Db 1851 AATGACGGCCAAATTTGACTACGCGGAATTTGTAGCATGATCAAGGCGAGCAACGTTGGA 1910

Qy 1471 GGGAGAAAGCAAGCCATGATGAAGAACTTTGAACATTTCAACATTTGCTGTGATGCTTTTGGAGTT 1530

Db 1911 CTAGGCTGGCAAAACAATGGAAGCAGTTTGAATGTAGCATTAAGAGACGCACTCAAGTA 1970

Qy 1531 GATGG 1535

Db 1971 CATTG 1975

RESULT 10
AAF74275
ID AAF74275 standard; DNA; 1910 BP.
XX AAF74275;
XX 04-MAY-2001 (first entry)
XX Sweet potato calcium dependent protein kinase clone.
XX Calcium dependent protein kinase; CDPK; herbicide resistance;
KW paraquat; diquat; crop production; ds.
XX Ipomoea batatas.
XX OS
XX WO200107592-A2.
XX 01-FEB-2001.
XX PD
XX 26-JUL-2000; 2000WO-GB02876.
XX PF
XX 27-JUL-1999; 99GB-0017642.
XX PR
XX (ZENE) ZENECA LTD.
XX PA
XX Holt CD, White AJ, Michael AJ, Osborn RW;
PI WPI; 2001-168549/17.
XX DR
XX Producing herbicide resistance plants by inhibiting calcium dependent
PT protein kinase in plants or by providing an intracellular vacuolar
PT transporter capable of transporting agrochemical into plant vacuole
XX Claim 18; Page 38; 50pp; English.
XX The present invention describes a method of producing plants which are
CC resistant to the herbicides paraquat and diquat, involving inhibiting in
CC the plants a calcium dependent protein kinase (CDPK) and selecting those
CC plants which are resistant to the agrochemical of interest. This is
CC useful in the production of crops with herbicide resistance.
XX Sequence 1910 BP; 560 A; 348 C; 481 G; 521 T; 0 other;

		Query Match	30.7%	Score 537.2	DB 22	Length 1910
		Best Local Similarity	63.2%	Pred. No. 6.8e-112		
		Matches 843	Conservative 0	Mismatches 488	Indels 3	Gaps 1
Qy	131	TAAGAGATCAATTAACCTCTCTGGGAAAAAGCTAGGCCAAGCCAAATTTGGAACAACCTATC 190				
Db	308	TTAGGGCACATTACAGTCTGGGAAAAAGACTGGGTAGGGGTCAATTTGGGGTTACCTATT 367				
Qy	191	TCTGCACAGAGAAATCAACCTCCGCTAATTACGGCTCAAAATCGATCCCGAAGCGAAAGC 250				
Db	368	TGTTGATCTGAGATTAGAACTGGAAGCAGTATGCTCTCAAGTCAATTTCCAGAAAAGC 427				
Qy	251	TCGTGTGCGGAGGATTAAGAGATGATAGCGGTGAGATTCAGATCATGCATCTCTCT 310				
Db	428	TTGTGACTAAGGGGATTAAGATGATAGGAGGAGGTTCAGATATATGCAGCACTGA 487				
Qy	311	CTGAGCATCAAAATGTTGTAGGATCAAAAGGACTTATGAAGATTCGGTGTGTTGTTCTATA 370				
Db	488	GTGGCAGCCCTAATATGTTGAGTTCAAGGGGCTTATGAGGATGCTAATTTCTGTGATC 547				
Qy	371	TTGTTATGGAGTTTGTGAAGTGGTGGAGCTTTTGTATCGGATGTTTCTAAAGTCAAT 430				
Db	548	TTGTGATGGAGTTGTGTGCTGGTGGAGAGCTTTTCGATCGGATTTATGCTAAGGGGCACT 607				
Qy	431	TTAGTGAGCGGTCAAGCTGTCAAGCTTATTAAGACGATCTTGTGTGTTGTTGAGGCTGTC 490				
Db	608	ATAGCGAAAGGCTGCTGCTCTCTTTGCAGGCTATAGTGAATGTTGTTCTATCTATCTGCC 567				
Qy	491	ATTCTCTTGGTGTATGCATAGAGATCTCAAACTCGAGATTTCTTTGTTGATGATCTCTA 550				
Db	668	ATTTATGGGCTGATGACCGGATTTGAAGCCCGAGAAATTTCTGTTCTGTCTGTATATAA 727				
Qy	551	AAGATGATCTAAGCTTAAGGCTACCGATTTTGGTGTGCTCTGCTTCTATAAGCCAGGAC 610				
Db	728	CTGAAAATGCTCCCTTGAAGGCTACTGATTTTGGCTTATCAGTGTTCATGGAAGAGGAA 787				
Qy	611	AATATTTATGAGCTAGTTGGAAGTCCGTAATACTGTTGACACAGAGGTGCTAAAGAAAT 670				
Db	788	GGGTGTATAGGATTTAGTCGGGAGTGTCTACTATGTTGCTCCCGAGGCTTGGGAGAA 847				
Qy	671	GTTATGGACCTGAAATAGATGTGGAGTGTGTTGTTATCTCTACATTTTACTCAGCG 730				
Db	848	AGTATGGAAGGAAGCGGATGTTTCGAGTGCAGGTGTTATGTTGTATATTTTACTCAGTG 907				
Qy	731	GTGTTCTCTCCCTCTGGGACAGACTGAGTCTGSAATCTTTAGACAGATATTCGAAGGA 790				
Db	908	GTGTGCTCTCCCTCTGGGCTGAACTGAGCGGGGATCTTTAATGCTATACTTAAAGGAG 967				
Qy	791	AGTTAGATTTCAAACTGACCGGTGGCTACTATCTCAGAAAGTGTCTAAAGATTTGATCT 850				
Db	968	AACTCGACTTCCAAACGAACCTTGGCTTCTATATCGAGCATTTGCCAAGGACCTAGTAC 1027				
Qy	851	ATAAATGCTCGAAGGAGCCCCAGAAACGATTTCTGCTCATGAGCCTTGTGTCACC 910				
Db	1028	GAGGATGCTAGCCCCAGACCCGAGAGAGCGCTTACTGCTGCCCGAGTTCCTGAGCATC 1087				
Qy	911	CATGATTTGTGATGAACAAGCAGCAGCAGCAAGCCCTTTGATCCAGCAGTCTTATCTC 970				
Db	1088	CATGATGCGAGAAGATGAGAAGCATCTGACAGACCACCTAGATAGCGCTTCTCTCAA 1147				
Qy	971	GTCTAAGCAGTTTCTCAATGAATAGATTAAGAAATGGCAATGGCATTCAGGGTAAATGCTG 1030				
Db	1148	GAATGAAGCAATTCAGAGCAATGAACAACTCAAGAACTTGGCCCTGAAGTTTATGTCAG 1207				
Qy	1031	AGAGACTTTCAGAGGAAGAAATTTGGAGTCTTGAAGGAATTTTCAAGATGATAGACACAG 1090				
Db	1208	AAAATCTCTCAGAAGAAGAAATTCATGACTGAAAGCAATGTTTCAAGATATCGACACTG 1267				
Qy	1091	ACACAGCGGAACGATTTCTTTGAAGAGCTCAAGCGGGTTTGAAGAGAGTTCGGATCTG 1150				
Db	1268	ACACAGTGGTACAAATTAATACGAAGAACTGAAGAGGGATTTGCCCAACTCGGGGCAA 1327				

Qy	1151	AACTGATGAATCAGAAATCAAGTCTCTCATGGATGCGGCTGATATCGACAACAGTGGTA 1210						
Db	1328	ATCTCAGAGGCTGAAGTTAAGCAGATTGATGGAAGCTGCTGATGTAGATGAAATGGCT 1387						
Qy	1211	CAATGACTACGAGAAATTCCTAGCAGCAACCTTACATGAACAAGATGGAGAGAGAGG 1270						
Db	1388	CGATGACTACATGNAATTCATCTGCTACATGCCAAGCAGAGCTAGAAGAGAG 1447						
Qy	1271	AGATTCTGGTGGCTGCAATTTTCGGAATTTTGACAAAGAGCGGAGGTTTATATCACCATCG 1330						
Db	1448	AAAATCTATACAAAGCAATTTTCAGTATTTTGTATTAAGATAGCAGTGGATTTATCAGAG 1507						
Qy	1331	ATCAGCTTCAGTCAAGCTTCACAGAGTTTGGTCTATGTGAT---ACACCTCTGGACGACA 1387						
Db	1508	ATGAATAGAGACTGCTATGAAGGACACGGATAGCTGATGCAGCACTATAAGGAAA 1567						
Qy	1388	TGATCAAGGAGATTGATCTTGACAAATGACGGGAAGATCGATTTCTCGAGTTTACAGAA 1447						
Db	1568	TAATATCTGAAGTCGATGCAGATCATGATGGAAGAAATCAACTATGAAGAGTTTTCACAA 1627						
Qy	1448	TGATGAGGAAAGGA 1461						
Db	1628	TGATGAGATCAGGA 1641						

RESULT 11
 ABA91081
 ID ABA91081 standard; cDNA; 2230 BP.
 XX
 AC ABA91081;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Physcomitrella patens CPK-2 full-length cDNA, SEQ ID NO:26.
 XX
 KW Protein kinase stress-related protein; PKSRP; moss; protein kinase-6;
 KW PK-6; protein kinase-7; PK-7; protein kinase-8; PK-8; protein kinase-9;
 KW PK-9; casein kinase homologue-1; CK-1; casein kinase homologue-2; CK-2;
 KW casein kinase homologue-3; CK-3; mitogen-activated protein kinase;
 KW MAP kinase-2; MPK-2; MAP kinase-3; MPK-3; MAP kinase-4; MPK-4;
 KW MAP kinase-5; MPK-5; calcium-dependent protein kinase-1; CPK-1;
 KW calcium-dependent protein kinase-2; CPK-2; overexpression;
 KW environmental stress; salinity; drought; temperature; tolerance;
 KW transgenic plant; EST; expressed sequence tag; ss.
 XX
 OS Physcomitrella patens.
 XX
 EN WO2001/7356-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-US11435.
 XX
 PR 07-APR-2000; 2000US-196001P.
 XX
 PA (BADI) BASF PLANT SCI GMBH.
 XX
 PI Da Costa Silva EO, Bohnert HJ, Van Thiel N, Chen R;
 PI Sarria-Millan R;
 XX
 DR WPI: 2002-049153/06.
 DR P-PSDB; AAM52842.
 XX
 PT New protein, useful for increasing tolerance to environmental stress,
 PT comprises a Protein Kinase Stress-Related Protein selected from
 PT Protein kinases, casein kinase homologs, MAP kinases or calcium
 PT dependent protein kinases -
 XX
 PS Claim 14; Fig 2M; 154pp; English.
 XX
 CC Sequences AAM52830-AAM52842 represent novel protein kinase stress-related
 CC proteins (PKSRPs) from the moss Physcomitrella patens, and sequences
 CC ABA91069-ABA91081 represent full-length cDNAs encoding them. The cDNA

CC sequences were obtained from expressed sequence tags (ESTs; ABA91056-
 CC ABA91058) derived from Physcomitrella patens cDNA libraries. The PKSRs
 CC of the invention comprise protein kinase-6 (PK-6), protein kinase-7
 CC (PK-7), protein kinase-8 (PK-8), protein kinase-9 (PK-9), casein kinase
 CC homologue-1 (CK-1), casein kinase homologue-2 (CK-2), casein kinase
 CC homologue-3 (CK-3), mitogen-activated protein (MAP) kinase-2 (MPK-2),
 CC MAP kinase-3 (MPK-3), MAP kinase-4 (MPK-4), and calcium-dependent protein
 CC kinase-2 (CPK-2). When overexpressed, the PKSRs are able to confer
 CC tolerance to environmental stresses such as salinity, drought,
 CC temperature, metal, chemical, pathogenic and oxidative stress.
 CC Physcomitrella patens PKSR nucleic acids may be used to generate
 CC transgenic plants and seeds with increased tolerance to salinity, drought
 CC and temperature. The transgenic plants generated can be monocots or
 CC dicots and are especially maize, wheat, rye, oat, triticale, rice,
 CC barley, cotton, rapeseed, cassava, sunflower, teagates, leguminous plants
 CC (e.g., soybean, peanut, Vicia species, alfalfa), solanaceous plants
 CC (e.g., potato, tobacco, aubergine, pepper, tomato), coffee, cacao, tea,
 CC Salix species, oil palm, coconut, perennial grasses and forage crops. The
 CC PKSR nucleotide and proteins may also be used in evolutionary and
 CC protein structural studies and as markers for specific regions of
 CC the genome.

XX Sequence 2230 BP; 572 A; 477 C; 661 G; 520 T; 0 other;

Query Match 30.4%; Score 531.8; DB 24; Length 2230;
 Best Local Similarity 62.5%; Pred. No. 1.2e-110;
 Matches 849; Conservative 0; Mismatches 507; Indels 3; Gaps 1;

QY 141 TTACCTTCTGGGAAAAAGCTAGGCGAAGGCAATTTGGAAACAACCTATCTCTGCACAGA 200
 DB 602 TTACATCTCTGGGACGGAGCTTGGCGAGGCGAGTTCGGAGTGACTTACTTGTGTACTGA 661
 QY 201 GAAATCAACCTCCGCTAATAGCCCTGCAATCGATCCGAGGGAAGCTCGTGTCTGC 260
 DB 662 CAAGATGACGAATGAGCGGTACCGCTGCAAGAGCATCCCAACGGAACTGACCACTAA 721
 QY 261 CGAGGATACGAGGATGATGCGGTGAGATTCAGATCATGATCATCTCTCTGAGCATCC 320
 DB 722 GNGGATATCGAGGATGTTAAGCGGAGGTTTCAGATTAATGATCATCACTGTCCGGGACAC 781
 QY 321 AATGTTGTAGATCAAGGAGCTTATGAGATTCGGTGTGTTGTTCTATATGTTATGGA 380
 DB 782 CAATATCGTGGTGTAAAGGATGTGTTCAGGACCAAGCATTCGGTGCATCTTGTGATGGA 841
 QY 381 GNTTGTGAGGTGGTGAAGCTTTTCATCGGATGTTCTTAAAGGTCAATTTAGTGAGCG 440
 DB 842 GCTCTGTGAGGTGGCGAGCTCTTCATCGCATATTGCCAAGGGGCATTACAGTGAGCG 901
 QY 441 TGAAGCTGTCAAGCTTATTAAGACGATCTTGGTGTGTTGAGGCTTGTCTCTCTCTGG 500
 DB 902 CGCGCTGCCGATATGCGAGATCATCGCTCAATGTGTCACACAGATCCCACTCAATAGG 961
 QY 501 TGTATGATAGAGATCTCAAACTCAGAAATTTCTGTTGATAGTCTCTAAAGATGATGC 560
 DB 962 GGTCTTCATCGGATCTCAAGCAGAGAAATTTCTGTTGGCCAGCAAGGCTGAGGATGC 1021
 QY 561 TAAGCTTAAGGCTACCGATTTGGTGTGTTGTTCTATATAAGCCAGGACAAATATTATA 620
 DB 1022 GCCTCTGAAGGCCACAGACTTCGGTCTGTCAACTTCTTTAAAGCCAGGAGATGTGTTCCA 1081
 QY 621 TGAGTGTAGTCCGCTACTACTGTTGACCCAGAGGTCCTAAAGAAATGTTATGGACC 680
 DB 1082 GGAATTTGGAAGTGGGATTTACGTGGCCCTGAAAGTTTGAAGAGAGATTAATGTTCC 1141
 QY 681 TGAATATAGATGTGGAGTGTGTTGTTATCTCTACATTTTACTCAGCGGTGTTCTCC 740
 DB 1142 TGAAGTGTATTTGGAGTGCAGCGGTGATTTGTATCTCTGCTGTGTGTGATACCC 1201
 QY 741 CTTCTGGCAGAGACTGAGTCTGAACTTTTAGACAGATTTCAAGGGAAGTTAGATT 800
 DB 1202 CTTCTGGGCTGAAACTGAGAGGGGTATCTTTGACGCTGTCTCAAGGGCACATAGACT 1261

QY 801 CAAATCTGACCGTGGCCTACTATCTCAGAGCTGCTAAAGATTGATCTATAAATGCT 860
 DB 1262 CGAAGACGATCCATGCGCCGAAATCTCAACGGGCTAAGATTGTTGTCAGGAAATGCT 1321
 QY 861 CGAAGGAGGCCCCCAAGAACGCAATTTCTGCTCATGAAGCCCTTGTGTACCCATGATGTT 920
 DB 1322 AAACCTAAGCTGAAGATACGTTCAAGSCACAGCAGGTGTTGAACCATCCATGGATGAA 1381
 QY 921 CGATGAACAGAGCAGCAGACCAAGCCCTTTCATCCAGCAGTCTTATCTCGTCTAAAGCA 980
 DB 1382 GGAAGATGTTGATGCTCCAGAGCTGCCACTCGCAATCGGTTGTTGACAGACTGAAAA 1441
 QY 981 GTTCTCTCAATCAATGAATTAAGAAAAATGGCAATTCGCGTAAATTCGTGAGAGACTTTC 1040
 DB 1442 TTCTCAGCCGCCCAACAAGATGAAAAGCTGGCTGAAGTGAATTCGAGAGAGTCTCTC 1501
 QY 1041 AGAGGAAGAAATTTGGAGTCTGAGGAATTTGTCAGATGATAGACAGACACAGAGCGG 1100
 DB 1502 GGAGGAAGAGATCGTGGGTTGAGGAGATGTTCAATCCATAGATACAGACACAGCGG 1561
 QY 1101 AACGATTACTTTTGAAGAGCTCAAGCGGTTTGAAGAGAGTCCGATCTGAACTGATGGA 1160
 DB 1562 CACGTCAGCTTCGAGAGCTTAAGGAAGGTTGCTGAAGCAGGGCTCAAAACTTAAATGA 1621
 QY 1161 ATCAGAAATCAAGTCTCTCATGGATCGGCTGATATCGACACAGTGGTACATAGACTA 1220
 DB 1622 ATCGACATCAGGAAACTAATGAAGCTGCAGATGTGATGGAACCGCAAGATCGACTT 1681
 QY 1221 CGGAGATTCCTACGACCAACCTTACACATGAACAAGATGGAGAGAGAGATTCCTGT 1280
 DB 1682 CAACGAGTTCTATTCGCAACAATGCACATGACAGACGAGAGAGAGATCCACCTTTG 1741
 QY 1281 GGCTGCAATTTTCGAGCTTTGACAAAGAGCGGATTTATATCACCATCGATGAGTCTCA 1340
 DB 1742 GCGACATTCATGATTCGACACGGAATAGACTACGAGGTATATCACCATCGAGGCTCA 1801
 QY 1341 GTCAGCTTGCACAGATTTGCTCTATCTGATAC---ACCTCTGGAGCAGATGATCAAGGA 1397
 DB 1802 GGAAGCAATGAGAGAAATGGAATGGAGATCTGAGACCATCCAGAGATCATCAGCGA 1861
 QY 1398 GATTGATCTTGACAAATGACGGGAAGATCGATTTCTCGGAGTTTACAGCAATGATGAGGA 1457
 DB 1862 GGTGACACAGACAAACGAGCGGAAGATAGACTACGAGGTTCGTAGCCATGATGCGCAA 1921
 QY 1458 AGGAGATGGAGTTGGAGAGACAGAACCATGATGAAGAA 1496
 DB 1922 GGGCAATCTCGCGCTGAAAACGGAGGAACGGTGAACAA 1960

RESULT 12

AAF74281
 ID AAF74281 standard; DNA; 1647 BP.

XX AAF74281;

DT 04-MAY-2001 (first entry)

XX Liverwort calcium dependent protein kinase clone #1.

XX Calcium dependent protein kinase; CDPK; herbicide resistance;
 KW paraquat; diquat; crop production; ds.

XX Marchantia polymorpha.

XX WO200107592-A2.

XX 01-FEB-2001.

XX 26-JUL-2000; 2000WO-GB02876.

XX 27-JUL-1999; 99GB-0017642.

XX (ZENE) ZENECA LTD.

XX Holt CD, White AJ, Michael AJ, Osborn RW;
 PI WPI; 2001-168549/17.
 DR
 XX Producing herbicide resistance plants by inhibiting calcium dependent
 PT protein kinase in plants or by providing an intracellular vacuolar
 PT transporter capable of transporting agrochemical into plant vacuole
 XX
 XX Claim 18; Page 42; 50pp; English.
 XX
 XX The present invention describes a method of producing plants which are
 CC resistant to the herbicides paraquat and diquat, involving inhibiting in
 CC the plants a calcium dependent protein kinase (CDPK) and selecting those
 CC plants which are resistant to the agrochemical of interest. This is
 CC useful in the production of crops with herbicide resistance.
 XX
 XX Sequence 1647 BP; 447 A; 349 C; 465 G; 386 T; 0 other;
 SQ

Query Match 29.9%; Score 523; DB 22; Length 1647;
 Best Local Similarity 62.7%; Pred. No. 1.1e-108;
 Matches 830; Conservative 0; Mismatches 490; Indels 3; Gaps 1;

QY 141 TTACCTTCGGGAAAAGCTAGCCAGGCGCAATTTGGAACAACCTATCTCTGCACAGA 200
 DB 240 TTACACCTTCGGGCGGAACCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 299
 QY 201 GAATCAACCTCCGCTAATTAGGCTCGAATCGATCCGAAGCGGAAGCTCGTGTGTCG 260
 DB 300 CAAGGTTACAGGTGAGCTTTTAGCCTCCAAAGTCAATTCGAAGGGAAGTTGACCAATAA 359
 QY 261 CGAGGATTACGAAGATGATGGCTGGAGATTCAGATCATGCATCATCTCTCTGAGCATCC 320
 DB 360 GGATGACGTAGGAGATGTCGGAGGAGTGCAGATCATGCACCATAGAGGGGCGAGAA 419
 QY 321 AAATGTTGTTAGGATCAAGGACCTATGAAGATTCGGTGTGTTGTCATATTTGTTATGA 380
 DB 420 GAACATTCGCAATTTGAAGGGGGCTATGAGGATAAACAACATGTCATCTCGTCATGGA 479
 QY 381 GTTTGTGCAAGGTGTGAGCTTTTGTATCGGATTTTCTAAAGGTCAATTTAGTGAGCG 440
 DB 480 GCTTGTGCTGGGAGAACTCTTCGACCGCATTTTCAGGGGGCCACTACAGTGNAG 539
 QY 441 TGAAGCTGTCAAGCTTATTAAGACGATTTGGTGTGTTGAGGCTTGTCAATCTCTCTGG 500
 DB 540 GGCTGTGCGAGCTCATGTAGAACTATAGTCAAGAGTGGTTCAGACGTGCCATCTCTGGG 599
 QY 501 TGTATGATAGATCTCAACCTGAGATTTCTGTGTTGATAGTCTCTAAAGATGATGC 560
 DB 600 AGTTATGACCGGGATCTGAAGCCGAGAAATTTCTGCTTCTCTCAAGCTCGAGAGGTTAC 620
 QY 561 TAAGCTTAAGGCTACCGATTTTGGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 680
 DB 660 ACCCTGGAAGCGACGGATTTTGGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 719
 QY 621 TGAAGTGTGAAGTCGCTACTATGTTGCAACGAGAGTGTCTAAAGAAATGTTATGAGCC 680
 DB 720 AGATATCGTGTGAAGTGTCTACTGTCGACCGACGAGGTTTGGTGTGTTGTTGTTGTTGTT 779
 QY 681 TGAATATAGATGTGTGAGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 740
 DB 780 AGAGGCTGATGTTGGAGTGTGCGAGTCAATCTTTTACATTTCTTTGTCGGAGTCCCTCC 839
 QY 741 CTCTCGGCGAGAGCTGAGTCTGGAACTCTTTAGACAGATATGCAAGGGAAGTTAGATTT 800
 DB 840 TTTCTGGGCGAGAAACCGAACAAAGGATTTTGTATGCCGTAATGCAAGGTCATATTTGATTT 899
 QY 801 CAAATCTGACCGCTGCGCTACTATCTCAGAGCTGCTAAAGATTTGATCTATAAAGTCT 860
 DB 900 CACTAGTATCTTGGCTTCAATTTCTCAAGGCGGAAGATCTGTTAAAGAGGATGCT 959
 QY 861 CGAAAGAGCCCCAAGAAACGATTTCTGCTCATGAAGCCTTGTGTACCCATGATGTT 920

DB 960 CAAAACAGAACCCAAAGGAGCGGATTGACGCCCATGAAGTTTTAGTCAACCCATGATTAG 1019
 QY 921 CGATGAACAGCAGCACCAGACAAGCCTTTGATCCACAGCTTTATCTGCTCTAAAGCA 980
 DB 1020 TGTGACGGAGAGGACACAGACAACCACTTGACAAACCCGTTGTCTAGATTGAAGCA 1079
 QY 981 GTTTTCTCAAAATGAATTAAGAAATGSCATTACGGGTAAATTTGTTGAGAGACTTTC 1040
 DB 1080 ATTACCGGTATGAACAGCTCAAGAACTTCTCTGAAGGTTATCGGACAGAGTCTCTC 1139
 QY 1041 AGAGGAAGAAATTTGGAGGTCTGAAGGAATTTGTTCAAGATGATAGACACAGACAGCGG 1100
 DB 1140 TGAAGAAGAGATCATGGATTGAAGGAGATGTTAAAGAGTATGGACACAGACAACAGTGG 1199
 QY 1101 AACGATTAATTTTGAAGAGCTCAAAAGCGGTTTGAAGAGAGTTCGGATCTGACTGATGGA 1160
 DB 1200 TACAATCACGTTTCGAGGAGTTGAAGATGCTTCTTCAAAGAGGAGATCAAACTTGGCAGA 1259
 QY 1161 ATCAGAAATCAAGTCTCTCATGATCGGCTGATATCGAACACAGTGTGTACATAGACTA 1220
 DB 1260 GTCAGAAGTGGCGCAGCTAATGSCAGCTCTGATGTGGATGCAATGGCACTATTGACTA 1319
 QY 1221 CGAGAAATTCCTAGCAGCAACCTTACACATGAACAAGATGGAGAGAGGAGATTTCTGGT 1280
 DB 1320 CTTGAGGTTTCATAACGGCAACCATGCACTTGAATGAATAGATAGAGAAAGATCATCTTTA 1379
 QY 1281 GGCTGCATTTTCGACATTTTGCACAAAGACGGAAGCGGTTATATCACCATCGATGAGCTTCA 1340
 DB 1380 CGCTGCCCTTTCAGCAATTTTGTAGGACAGCAGTGGTTCATCACCATGGAAGAGCTTGA 1439
 QY 1341 GTCAAGCTTGACAGAGTTTGGTCTATGTGATAC---ACCTCTGGAGCAGATGATCAAGGA 1397
 DB 1440 ACAGGCTTTAATTAAGCACGGGATGGAGATCTCTGATCTCTGAAAGAAATTTATTAGGGA 1499
 QY 1398 GATTGATCTTGACAAATGACGGGAAGATCGATTTCTCGGAGTTTACAGCAATGATGAGGAA 1457
 DB 1500 GTTTGACACTGATCATGATGAGCAATCAACTACGAGAGTTCGTTGCCATGATGCGTAA 1559
 QY 1458 AGG 1460
 DB 1560 AGG 1562

RESULT 13
 AAF74270
 ID AAF74270 standard; DNA; 1791 BP.
 XX
 XX AAF74270;
 XX
 XX
 DT 04-MAY-2001 (first entry)
 DE Carrot calcium dependent protein kinase clone.
 XX
 XX Calcium dependent protein kinase; CDPK; herbicide resistance;
 KW paraquat; diquat; crop production; ds.
 XX
 XX Daucus carota.
 XX
 PN WO200107592-A2.
 XX
 PD 01-FEB-2001.
 XX
 XX 26-JUL-2000; 2000WO-GB02876.
 PF
 XX 27-JUL-1999; 99GB-0017642.
 PR
 XX (ZENE) ZENECA LTD.
 PA
 XX Holt CD, White AJ, Michael AJ, Osborn RW;
 PI WPI; 2001-168549/17.
 XX
 XX Producing herbicide resistance plants by inhibiting calcium dependent

protein kinase in plants or by providing an intracellular vacuolar transporter capable of transporting agrochemical into plant vacuole

Claim 18; Page 34-35; 50pp; English.

The present invention describes a method of producing plants which are resistant to the herbicides paraquat and diquat, involving inhibiting in the plants a calcium dependent protein kinase (CDPK) and selecting those plants which are resistant to the agrochemical of interest. This is useful in the production of crops with herbicide resistance.

Sequence 1791 BP; 554 A; 286 C; 448 G; 503 T; 0 other;

Query Match 29.9%; Score 522.8; DB 22; Length 1791;
Best Local Similarity 61.8%; Pred. No. 1.2e-108;
Matches 869; Conservative 0; Mismatches 527; Indels 9; Gaps 2;

QY 61 CCAAAATGGAGCAAGCAACCTAGAGCTGCTTCAACACAGATTACCATATCAA 120
Db 251 CTTTCACTTAAGCCAGGCAAGTTTCATAGAGCTGATCAACACACTATTTTAGSCAAGCCA 310
QY 121 ACACACAGATTAAAGAGATCATACCTCTGGGAAAAAGCTAGGCCAAGGCAATTTGGA 180
Db 311 TTGGAAGATTAGGGGTAAGTATCTCTTGGGAAGAAATTGGCGAGGGTCAATTTGGT 370
QY 181 ACAACCTATCTCTGACACAGAGAAATCAACCTCCGCTAANTACGCTGCAATCGATCCCG 240
Db 371 TGTGTATATCAATGTACTGAGAATTCAAGTGTCTCAATTTATATGCTTGAAGTCTATTTTA 430
QY 241 AAGCGAAGCTGCTGTCGCGAGATTACGAAGATGATGCGGTGAGATTCAGATCATG 300
Db 431 AAGAGAAAGCTTGTAGTAAGAAATGATAGGAGGATTAAGAGGGAGATTCAAGATTTG 490
QY 301 CATCATCTCTGAGCATCCAAATGTGTAGGATCAAGGGAGCTTATGAAGATTCGGTG 360
Db 491 CAGCAATTTGAGTGGCAACCGAATATTTGGAGTTTAAAGTGTTTTGGAGATAGGCAA 550
QY 361 TTTGTTTATATTGATGAGGTTTGTGAAGTGTGAGCTTTTGTGCGATTGTTTCT 420
Db 551 TCTGTGCACCTTGTGATGAGCTTTGTGCTGGGGAGTTGTTTGACAGGATTTATAGCT 610
QY 421 AAAGGTCAATTTAGTGAGCGTGAAGCTGCAAGCTTATTAAGACGATTCCTTGGTGTGTT 480
Db 611 CAGGACATTTACTCGAGAGAGCGGCTGCTACGATTTGAGCAGATTTGTAATGTTGTC 670
QY 481 GAGGTTGCAATCTCTTGGTGTATGATAGATGATCAACCTGAGAATTTCTTGT 540
Db 671 CATGTTGTCAATTTATGGGGGTGATGCTAGAGGATCTTAAAGCCTGAAAATTTCTTGT 730
QY 541 GATAGTCTTAAAGATGATGCTAAGCTTAAAGGTACCGATTTTGGTGTGCTCTCTAT 600
Db 731 TCGAGTAAGGATTAAGATGCAATGCTGAAGGCGACGATTTTCGGGTATCTGCTTCATT 790
QY 601 AAGCCAGCAATATTATATGACGTAGTTGGAAGTCCCTACTATGTTGCCACAGAGTG 660
Db 791 GAAGAGAAAGGTATATCTGTAATATAGTTGGTAGTCTTACTATGTTGCTCCTGAAGTA 850
QY 661 CTAAAGAAATGTTATGACCTGAATAGATGCTGGAGTGGTGTATCTCTCTACATT 720
Db 851 CTACAGCTAGTTATGAAGAGAGATTGATCTGAGCGCTGGAGTTATTTGATATA 910
QY 721 TTACTCAGCGGTGTTCTCCCTTCTGGGACAGAGCTAGTCTGGAATCTTTAGACAGATA 780
Db 911 CTACTTAGCGGGGTACCTCCATTTTGGGACAGAAATGAAAAGGAATATTTGATGCAATA 970
QY 781 TTGCAAGGAAGTTAGATTCAATCTGACCCGTGCGCTACTATCTCAGAAGCTGTAAA 840
Db 971 CTGAAGAGGATGATTGACTTTGAAAGTGAACCATGGCCATCAGTCTCAACAGTGCAPAA 1030
QY 841 GATTITGATCTATAAAATGCTCGAAGAGAGCCCAAGAAAGCGCATTTTCTCTCATGAAGCC 900
Db 1031 GACCTTGTTGAAGAGATGCTGACACAGGATCCAAGGAGAGGATTTACTTCTGCAAGATT 1090

QY 901 TTGTGTCAACCCATGGATTGTCGATGAACAAAGCAGCAGCAGCAAGCCTCTTTGATCCACA 960
Db 1091 CTTGATCATCCCTGGATGAGAGAGGTGGAAGCATCAGACAAGCCAATAGATATGCA 1150
QY 961 GTCTATCTCGCTTAAAGCAGTTTTCTCAAATGAATGAATTAAGAAATGCAATACGG 1020
Db 1151 GTCTCTCTCTAGAAATGAAGCAGTTTCAGAGCAATGAACAGCTCAACCACTTGCATTAA 1210
QY 1021 GTAAATCTCAGAGACTTTTCAGAGAGGAAGAAATTTGGAGGTCTCTGAAGGAATTTTCAAGATG 1080
Db 1211 GTATCTGCTGAAGTCTATCCGAGGAGAAATTTAAAGGTCCTTAATCCATGTTTGCAAAC 1270
QY 1081 ATAGACACAGACAACAGCGGAACGATTAATCTTTGAAGAGCTCAAGCGGGTTTGAAGAGA 1140
Db 1271 ATGACACGCGACAAAAGTGTGTACATCACTTTATGAGGAATTTGAAATCAGGTTTGGCAGCG 1330
QY 1141 GTCCGATCTGAATCTGATGGAATCAGAAATCAAGTCTCTCATGATGCGGCTGATATCGAC 1200
Db 1331 CTAGCTCAAGCTATCAGAAATGAGGTCACAAATTTGATGATGCTCTGCTGATGTAGAT 1390
QY 1201 AACAGTGTCAATAGACTACGGAGAAATTCCTAGCAGCAACCTTACACATGAACAGATG 1260
Db 1391 GGAATGCTCAATTTGACTTACCTTGAATTTTACTGCTACTATGATAGGCAAGCTT 1450
QY 1261 GAGAGAGAGGAGATTCGTGGCTGCAATTTTCGAGCTTTGACAAAGCAGGAGCGGTTAT 1320
Db 1451 GAAAGTTATGAGCATC-----AAGCATTTTCAATTTTTCAGCAAGGATTAAGCGGCTTC 1504
QY 1321 ATCCATTCGATGAGCTTCAGTCAAGCTTTCAGCAGAGTTTGGTCTATGT---GATACACT 1377
Db 1505 ATTCTAAGATGAATCTGGAATCTGCAATGAAAGAGTATGAAATGGGTGACGAAGCCACT 1564
QY 1378 CTGGACGACATGATCAAGGAGATTGATCTTGACAATGACGGGAAGATCGATTTCTCGGAG 1437
Db 1565 ATCAAGGACATAATCTCTGAAGTAGATTCAAGTAATGATGGAAGGATTAATTAAGATGAG 1624
QY 1438 TTTACAGCAATGATGAGGAAAGGA 1461
Db 1625 TTCTGTGCGATGATGAGAAGGCA 1648

RESULT 14
AAF74284
ID AAF74284 standard; DNA; 2363 BP.
XX
AC AAF74284;
XX
DT 04-MAY-2001 (first entry)
XX
DE Common ice plant calcium dependent protein kinase clone.
XX
KW Calcium dependent protein kinase; CDPK; herbicide resistance;
paraquat; diquat; crop production; ds.
XX
OS Mesembryanthemum crystallinum.
XX
PN WO200107592-A2.
XX
PD 01-FEB-2001.
XX
PF 26-JUL-2000; 2000WO-GB02876.
XX
PR 27-JUL-1999; 99GB-0017642.
XX
PA (ZENE) ZENECA LTD.
XX
PI Holt CD, White AJ, Michael AJ, Osborn RW;
XX
DR WPI; 2001-168549/17.
XX
PT Producing herbicide resistance plants by inhibiting calcium dependent
protein kinase in plants or by providing an intracellular vacuolar
transporter capable of transporting agrochemical into plant vacuole

XX
PS
XX
CC
CC
CC
CC
CC
XX
SQ

Claim 18; Page 43-44; 50pp; English.

The present invention describes a method of producing plants which are resistant to the herbicides paraquat and diquat, involving inhibiting in the plants a calcium dependent protein kinase (CDPK) and selecting those plants which are resistant to the agrochemical of interest. This is useful in the production of crops with herbicide resistance.

Sequence 2363 BP; 718 A; 435 C; 542 G; 668 T; 0 other;

Query Match 29.9%; Score 521.6; DB 22; Length 2363;
Best Local Similarity 60.3%; Pred. No. 2.5e-108;
Matches 898; Conservative 0; Mismatches 584; Indels 6; Gaps 2;

74 CGAAGCCAAACCTAGACGCTCTTCAAAACACAGTCTTACCATATCAAAACACACACGATTA 133
Db 523 CAHAACAGCCCAAGAGTTGAGCCAAATACAAATTTGGTAAACCCCTTTGAGGATGTA 582
Qy 134 GAGATCAATTAACCTTGGGAAACAAAGCTAGGCCAAGCCAAATTTGGAAACACCTATCTCT 193
Db 583 AGGTGTACTACAACTTGGGAGAGAACTGGGTAGGGGTCAATTTGGGGTTACCTATCTGT 642
Qy 194 GCACAGAGAATCAACCTCGCTCAATTAACGCTGCAATCGATCCGAGGAGAAAGCTCG 253
Db 643 GCACAGAAAAGACTGGCCAAACATATGCTTGCAGTCAATCTCTAAGAGAGCTTG 702
Qy 254 TGTGTCGAGGATTAACGAGATGATAGCGGTGAGATTGAGATCAATCTCTCTCTCTG 313
Db 703 TGACCAAGGCTGATAGGATGATGAGGAGAGATTCAGATCATGTCAGGCATATGAGTG 762
Qy 314 AGCATCAATGTTGTAGGATCAAAAGGACTTATCAAGATTCGGTGTGTTGTTCAATTTG 373
Db 763 GTCAACCTAATTTGGAATTTAAGGGTCTTATGAGGATTAACACATCTGTGAATCTTG 822
Qy 374 TTATGGAGTTTGTGAAGGTGAGCTTTTATCGATCGATGTTTCTTAAAGTCAATTTA 433
Db 823 TGATGGAGCTTTGCTGTGGGAGTTGTTGATAGGATTTATGTAAGGGCCATTATA 882
Qy 434 GTGAGCGTGAAGCTGCAAGCTTATTAAGACGATTCCTGGTGTGTTGAGGCTGTGCAAT 493
Db 883 GTGAAAAGGCTGCTGCCACTATGTTGAGGAGATTTGTTAAGTTGTTTCAATGTTGCTACT 942
Qy 494 CTCCTGTGTTTATGATAGATCTCAAACTCGAGATTTCTTGTGTTGATGCTCTAAAG 553
Db 943 TTATGGGTGTGATGATAGGATCTGAAGCTCGAGAACTTCTGCTCTAGCAAGGATG 1002
Qy 554 ATGATGCTAAGCTTAAGCTACCGATTTGGTGTGCTGCTCTGATAGCCAGGACAT 613
Db 1003 AGAATCTCTCTTGAAGGCCACTGATTTGGGTGCTGCTGTTTATGAGAGGTTAAG 1062
Qy 614 ATTTATATGAGTGTGGAAGTCCGCTACTATGTTGACCCAGAGGTGCTAAAGAAATGTT 673
Db 1063 TCTACCGGATATAGTAGGAGTGTCTTACTATGCTGCTCTGAGGATTTGCGTGTAGT 1122
Qy 674 ATGACCTGAAATAGATGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 733
Db 1123 ATGGAAGGAGATTTGATTTGGAGTCTGAGTCTGATGTTGTTGATGCTTACTCAGTGTG 1182
Qy 734 TTCTCTCTCTCTGCGGAGAGACTCAGTCTGGAATCTTTAGACAGATATTGCAAGGAGT 793
Db 1183 TGCCCCCTTTTGGGCAACACGAGAAAGGATCTTTGATGCTATTTTGAAGGCCATA 1242
Qy 794 TAGATTTCAAACTGACCCGTGGCTACTATCTCAGAGCTGCTAAAGATTTGATCTATA 853
Db 1243 TTGATTTGAAAGCAACCAATGGCCATCAATTTCAATTTGTTGCTCAAGGACCTAGTGAGAA 1302
Qy 854 AAATGCTGAAAGAGAGCCCAAGAAAGCATTCTGCTCATGAAGCTTGTGTCACCCAT 913
Db 1303 AAATGTTGACAGAGATCCCAAGAAAGGATTTGCTGCTCAAGTCTTCTGAGCACCCAT 1362
Qy 914 GGATTTGATGAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 973

Db 1363 GGCTAAGAGATGGTGAAGCAT---CAGACAAAGCCAAATAGACAGTGTGTTCTCTCTCAGGA 1419
Qy 974 TAAAGCAGTTTTTCTCAAAATGAATTAAGAAATAGCATTACGGGTAAATTTGCTCTGAGA 1033
Db 1420 TGAAGCAATTCAGAGTCTATGAACAGCTCAAGAGCTCGCTCTAAGAGTCAATTTGCTGAAA 1479
Qy 1034 GACTTTAGAGGAATTTGGAGTCTGAGGATTTGTTCAAGATGATAGACACAGACA 1093
Db 1480 ATCTTTCTCTGATGAAGAGATCCAAAGGCTGAAACAAATGTTCCGGAATATGGACACTGATG 1539
Qy 1094 ACAGCGGAACGATTAATTTTGAAGAGCTCAAGCGGTTTGAAGAGAGTGGGATCTGAAC 1153
Db 1540 GTAGTGGGTCAATTAATTTAGAGACTGAGGAGGATTTGGCTCGACTTGGATCAAGC 1599
Qy 1154 TGATGAATCAGAAATCAAGTCTCTCATGGATGCGGCTGATATCGAACACAGTGTGACAA 1213
Db 1600 TTACTGAACTGAAGTGAAGCGCTCATGGAAGCTGCTGATCAAGATGGAAGTGGATCAA 1659
Qy 1214 TAGACTAGCGGAATTTCTAGCAGCAACCTTACACATGAAACAGATGGAGAGAGGAGA 1273
Db 1660 TAGACTATGATGTTCAATTAAGCCCAATTCATAGGTACAGTTAGAGAGATGAGC 1719
Qy 1274 TTCTGGTGGCTCATTTTGGAGCTTTGACAAAGCAGGAGCGGTTATATCACCATCGATG 1333
Db 1720 ATCTTTACAAGGCAATTCCTCAATATTTTCGACAAAGCAATAGTGGGTTTATCACAACAGATG 1779
Qy 1334 AGCTTCAGTCAGCTTGCAGAGATTTGCTGCTATGTGAT---ACACCTCTGGACGACATGA 1390
Db 1780 AACTGAAACAGCAATGAAGATGATGGATGCTGATGAGAAATTCATTTGCATTCAGAGATAT 1839
Qy 1391 TCAAGAGATTTGATCTTGAATAGCGGAAAGATGATTTCTCGAGTTTACAGCAATGA 1450
Db 1840 TGTGGAAGTGAACACTGATATGATGAAGAAATAAATATGATGAGTTCAAGTTCAGCGCAATGA 1899
Qy 1451 TGNAGGAAGAGATGGAGTTCGGAGAGCAGAACCATGATGAAGAACTTGAACCTCAACA 1510
Db 1900 TGAGAAGTGGGACTCAAAACCCGGTTACCAACTCATTTAGTGTGATGTCATGTCATGCTAGCA 1559
Qy 1511 TTCTCTGATGCTTTTGGAGTTGATGTTGAAATCTGATGACTGACTCA 1558
Db 1960 CTGTATACGTAAACGCTTTTAAAGTACCAGGGTATTGAACAGTCA 2007

RESULT 15
AAF74273
ID AAF74273 standard; DNA; 2436 BP.
XX
AC AAF74273;
XX
DT 04-MAY-2001 (first entry)
XX
DE Soybean calcium dependent protein kinase clone #1.
XX
KW Calcium dependent protein kinase; CDPK; herbicide resistance;
KW paraquat; diquat; crop production; ds.
XX
OS Glycine max.
XX
FN WO200107592-A2.
XX
PD 01-FEB-2001.
XX
PF 26-JUL-2000; 2000WO-GB02876.
XX
PR 27-JUL-1999; 99GB-0017642.
XX
PA (ZENE) ZENECA LTD.
XX
PI Holt CD, White AJ, Michael AJ, Osborn RW;
XX
DR WPI; 2001-168549/17.
XX
PT Producing herbicide resistance plants by inhibiting calcium dependent

Job time : 398 secs

Job time : 398 secs

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OM nucleic - nucleic search, using sw model

Run on: February 13, 2003, 17:50:37 ; Search time 75 Seconds
(without alignments)
7143.524 Million cell updates/sec

Title: US-09-848-806-2

Perfect score: 1747

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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 - 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
 - 3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
 - 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
 - 5: /cgn2_6/ptodata/2/ina/6C_COMB.seq:*
 - 6: /cgn2_6/ptodata/2/ina/6D_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	429.8	24.6	1349	1	US-07-951-715A-20
2	429.8	24.6	1349	2	US-08-459-448A-20
3	429.8	24.6	1349	3	US-08-459-595A-20
4	429.8	24.6	1349	4	US-08-459-504B-20
5	429.8	24.6	1349	5	US-08-459-444-20
6	429.8	24.6	1349	6	US-09-547-422-20
7	218	12.5	4162	2	US-08-459-448A-26
8	218	12.5	4162	3	US-08-459-595A-26
9	218	12.5	4162	3	US-08-459-504B-26
10	218	12.5	4162	3	US-08-459-444-26
11	218	12.5	4162	4	US-09-547-422-26
12	218	12.5	4165	1	US-07-951-715A-26
13	189.6	10.9	2374	4	US-09-347-801-3
14	165	9.4	1400	1	US-08-464-164-1
15	165	9.4	1400	1	US-08-338-057-1
16	165	9.4	1400	2	US-08-668-416-1
17	129.8	7.4	1776	3	US-08-655-352-10
18	129.8	7.4	1776	4	US-09-258-016-10
19	129.8	7.4	1776	4	US-09-257-825B-10
20	117	6.7	2061	4	US-09-800-960-1
21	114	6.5	2514	3	US-08-655-352-1
22	114	6.5	2514	4	US-09-258-016-1
23	114	6.5	2514	4	US-03-257-825B-1
24	104.2	6.0	1282	2	US-08-878-989-12
25	104.2	6.0	1282	4	US-08-272-796-12
26	98.2	5.6	3471	2	US-08-715-568A-2
27	92.6	5.3	498	4	US-09-347-801-7

Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 4, Appli
Sequence 9, Appli
Sequence 37, Appli
Sequence 36, Appli
Sequence 3, Appli
Sequence 44, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 3, Appli
Sequence 7, Appli

ALIGNMENTS

RESULT 1

US-07-951-715A-20

; Sequence 20, Application US/07951715A

; Patent No. 5625136

; GENERAL INFORMATION:

; APPLICANT: Koziel, Michael G.

; APPLICANT: Desai, Nalini M.

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; APPLICANT: Kramer, Vance C.

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; APPLICANT: Launis, Karen L.

; APPLICANT: Rothstein, Steven J.

; APPLICANT: Bowman, Cindy G.

; APPLICANT: Dawson, John L.

; APPLICANT: Dunder, Erik M.

; APPLICANT: Pace, Gary M.

; APPLICANT: Suttie, Janet L.

; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED

; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE

; NUMBER OF SEQUENCES: 94

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CIBA-GEIGY Corporation

; STREET: 7 Skyline Drive

; CITY: Hawthorne

; STATE: New York

; COUNTRY: USA

; ZIP: 10532

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.30B

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/951,715A

; FILING DATE: 25-SEP-1992

; CLASSIFICATION: 800

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/772,027

; FILING DATE: 04-OCT-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Spruiell, W. Murray

; REGISTRATION NUMBER: 32,943

; REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (919)541-8615

; TELEFAX: (919)541-8689

INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 1349 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
NAME/KEY: CDS
LOCATION: 3..1226 /note= "cDNA sequence for maize
OTHER INFORMATION: pollen-specific calcium dependent protein kinase gene as
OTHER INFORMATION: disclosed in Figure 30."
US-07-951-715A-20

Query Match 24.6%; Score 429.8; DB 1; Length 1349;
Best Local Similarity 60.3%; Pred. No. 1.4e-99;
Matches 729; Conservative 0; Mismatches 477; Indels 3; Gaps 1;

QY 290 TTCAGATCATGATCTCTCTGAGCATCCAAATGTTGTAGGATCAAGGACTTATG 349
Db 1 TGCAGATCATGACACCTCTCCGGCAGCCCAACGTTGGTGGCCCTCGCGGCGGTACG 60
QY 350 AAGATTCGGTGTGTTTCATATGTTATGAGAGTTTGTGAAGTGTGAGCTTTTGTGTC 409
Db 61 AGGACAAGCAGAGCGTGACCTCTCATGAGCTGTGCGCGGGGGAGCTCTTCGACC 120
QY 410 GGATTTGTTTAAAGGTTCATTTTAGTAGCGTGAAGGTGTCAAGCTTATTAAAGACGATTC 469
Db 121 GCAATCATGCCCGGGCCAGTACACGAGCGCGCGCGGAGCTCTCGCGGCCATCG 180
QY 470 TTGGTGTGTTGAGGCTGTCTATTCTTTGTTGTTATGATAGATCTCAAACCTTGAGA 529
Db 181 TGCAGATCGTGACACCTGCACTCCATGGGGTGATGACCGGGAGCATCAAGCCCGAGA 240
QY 530 ATTCTTGTGTTGATGCTCTAAAGATGATGTAAGCTTAAGCTTAAAGCTTGTGTTGT 589
Db 241 ACTTCTGCTGTCTAGCAAGGACGAGGAGCGCGCTCAAGCCACGACTTCGGCTCT 300
QY 590 CTGCTCTTATAAGCCAGGACATATTTATATGAGTGTGTTGAGTGTGAGTGTGTTG 649
Db 301 CGTCTCTTCAAGGAGGCGAGCTGCTCAGGACATCGTCCGAGCGGCTTACTACATCG 360
QY 650 CACGAGGTCTAAAGAAATGTTATGAGTCTGAATAGTGTGAGTGTGAGTGTGTTGTTA 709
Db 361 CGCCGAGTGTCTAAGAGGAAGTACGGCCCGGAGCGGAGTCTGAGAGCTCGGGTCA 420
QY 710 TCCTCTACATTTTACTCAGCGGTGTTCTCTCCCTTCTGGGCGAGACTGAGTCTGGAATCT 769
Db 421 TGCTCTACATCTCTCTCGCGGGTCTCTCCCTTCTGGGCGAGAAACGAGACGCGATCT 480
QY 770 TTAGACAGATTTGCAAGGAGTGTAGATTTCAATCTGACCGGTGCTACTATCTCAG 829
Db 481 TCACCGCATCTCTGCGAGGCGAGCTGAGCTCTCAGCGAGCGATGGCCACATCTCGC 540
QY 830 AAGCTGCTAAGATTTGATCTATAAATGCTCGAAGAGGCGCCCAAGAAAGCGATTTCTG 889
Db 541 CGGAGCCAGATCTCGTCAAGAGATGCTCAACATCAACCCCAAGAGGCGGTCAAGG 600
QY 890 CTCAATGAGCTTGTGTCACCCATGATTTGATGAACAGCAGCACCAGACAGGCTTC 949
Db 601 CGTTCAGGTCCTCAATCAACCCATGATCAAAAGAGCAGGAGCGGCTGACAGCGCGC 660
QY 950 TTGATCCAGAGCTTATCTGCTTAAAGCAGTTTCTCAATGAATGAATTAAGAAAAA 1009
Db 661 TTGACAGCTTGTCTCGACAGGCTCAAGAGTTCAGGCGCATGACAGTTCAGAGAAAG 720
QY 1010 TGGCAATTCGGGTAATTTGTGAGAGCTTTTCAGAGGAAGAAATTTGAGTCTGAAGGAT 1069
Db 721 CAGCAATTTGAGGATCATAGCTGGTGGCTATCCGAGAGGAGATCAAGGGCTGAAGGAA 780
QY 1070 TGTTCAAGATGATAGACAGACAGACGAGCGGAACGATTACTTTTGAAGAGCTCAAGGCG 1129

Db 781 TGTTCAAGAACATTGCAAGGATACAGCGGACCAATTACCTTCGAGAGCTCAACACG 840
QY 1130 GTTTGAAGAGAGTCGATCTGAATGATGGAATCAGAATCAAGTCTCTCATGGATCGG 1189
Db 841 GGTTCGAAGACACGGGCCAAGCTGTGAGACAGGAATGGAGAACTAATGGAAGCAG 900
QY 1190 CTGATATCGACAACAGTGTGTAACAATAGACTACGAGAAATTCCTAGCAGCAACCTTACACA 1249
Db 901 CTGACGCTGACGCAACAGGCTTAAATTGACTACGACGAATTCGTACCGCAACAGTGCATA 960
QY 1250 TGAACAAGATGAGAGAGAGGAGATTCTGGTGGCTGCAATTTTCGACTTTGACAAAGACG 1309
Db 961 TGAACAACCTGGATAGAGAGAGCACCCTTACAGACATTCAGTATTTTCGACAAGGACA 1020
QY 1310 GAAGCGGTTATATCACCATCGATGAGCTTCAGTCTGACAGAGTTTGGTCTATGTC 1369
Db 1021 ACAGCGGTACATTACTTAAAGAAGAGCTTGAGCAGCCTTGAAGGAGCAAGGTTGTATG 1080
QY 1370 ATACACT---CTGGAGCAGCATGATCAAGGAGATGATCTTCACAATCAGGGAAGATCG 1426
Db 1081 ACGCCGATAAAATCAAGACATCATCTCCGATGCCGACTCTGACATGATGGAAGATAG 1140
QY 1427 ATTCTCGAGTTTACAGCAATGATGAGGAAAGGAGATGAGATTGGGAGAGCAACAA 1486
Db 1141 ATTATTCAGATTTTGGCGATGATGAGGAAGGAGCGCTGGTCCGAGCCATGAACA 1200
QY 1487 TGATGAAGA 1495
Db 1201 TCAAGAAGA 1209

RESULT 2
US-08-459-448A-20
Sequence 20, Application US/08459448A
Patent No. 5859336
GENERAL INFORMATION:
APPLICANT: Kozziel, Michael G.
APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lytle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Launis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESS: No. 5859336artis Corporation
STREET: Patent & Trademark Dept., 520 White Plains
STREET: Rd., POB 2005
CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591-9005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,448A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 800

Query Match	24.6%	Score 429.8	DB 2	Length 1349	
Best Local Similarity	50.3%	Pred No. 1.4e-99			
Matches 729	Conservative	0	Mismatches 477	Indels 3	Gaps 1
QY	290	TTGAGATCATGCAATCTCTCTGAGCATCCAAATGTTTGGATAGTCAAGGCACTTATG	349		
DB	1	TGAGATCATGCACCACTCTCCGGCAGCCCAAGCTGTGGGCCCTCCCGCGCGGTAGC	60		
QY	350	AAGATTCCGGTGTGTTGATATTGTTATGAGAGTGTGTAAGGTGTGAGCTTTTGTATC	409		
DB	61	AGGACAAGCAGACGCTGCACCTCGTCAATGAGCTGTGCGCGGCGGGAGCTCTTCGACC	120		
QY	410	GGATTGTTTCTAAAGTCTATTTAGTGAAGGTCAAGCTGTCAAGCTTATTAAAGACGATTC	469		
DB	121	GCATCATCGCCCGGGCCAGTACACGAGCGCGCGCCGCGGAGCTGTGCGGCCCATCG	180		
QY	470	TTGGTGTGTGAGGGTTGTCATTCCTCTGGTGTATGCAATAGAGATCTCAAAACCTGAGA	529		
DB	181	TGCAGATCGTGCACACCTGCGCACTCCATGSGGGTGATGCACCGGAGACATCAAGCCCGAGA	240		
QY	530	ATTCTCTGTTTGTATGATGCTTAAAGATGATCTTAAGCTTAAGGCTACCGATTTTGGTTTGT	589		
DB	241	ACTCTCTGCTCTCAGCAAGGACGAGACGCGCGCTCAAGGCCACCGACTTCGGCCCTCT	300		
QY	590	CTGTCTTCTATAGCCAGGACATATTTATATGACGTAGTTGGAAGTCCGTACTATGTTG	649		
DB	301	CCGTCCTTCTTCAAGGAGGGCGAGCTGCTCAGGAGACATCGTCGGAGCGGCTACTACATCG	360		
QY	650	CACCAGAGGTGCTAAAGAAATGTTATGAGCTGAAATAGATGTGTGAGTGTGCTGTTA	709		
DB	361	CGCCGAGGTGCTCAAGAGGAAGTACGCGCCCGAGGCGGACATCTGGAGCGTCGGGCTCA	420		
QY	710	TCCTCTACATTTTACTCAGCGGTGTTCCCTCCCTCTCGGCAGAGACTGAGTCTGGAATCT	769		
DB	421	TGCTCTACATTTCTCTGCGGGCTGCTCCCTTCTGGGACAGAACAGAAAGGCATCT	480		
QY	770	TTAGACAGATATTGCAAGGGAAGTTAGATTTCAAATCTGACCGGTGGCCCTACTATCTCAG	829		
DB	481	TCACCGGCATCTCGAGGGCAGCTTGACCTCTCCAGCGAGCCATGGCCACATCTCCG	540		
QY	830	AAGCTGCTTAAAGATTGATCTATAAAATGCTCGAAAGAGCCCCCAAGAAACCGCATTTCTG	889		
DB	541	CGGAGCCAAAGATCTCGTCAAGAAGATGCTCAACATCAACCCCAAGAGCGGCTCACGG	960		

RESULT 3
US-08-459-595A-20
; Sequence 20, Application US/08459595A
; Patent No. 6019104
; GENERAL INFORMATION:
; APPLICANT: Kozielec, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Lounis, Karen L.
; APPLICANT: Rothsstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary W.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNAA
; TITLE OF INVENTION: INSECTICIDAL
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6019104artis Cor
; STREET: Patent & Trademark Dept
; STREET: Rd., POB 2005

CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591-9005
COMPUTER: IBM PC compatible
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICANT: Patentin Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/459,595A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 800
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: 40403
REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8582
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 1349 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
FEATURE:

NAME/KEY: CDS
LOCATION: 3..1226
OTHER INFORMATION: /note= "cDNA sequence for maize
OTHER INFORMATION: pollen-specific calcium dependent protein kinase gene as
OTHER INFORMATION: disclosed in Figure 30."
US-08-459-595A-20

Query Match 24.68; Score 429.8; DB 3; Length 1349;
Best Local Similarity 60.34; Pred. No. 1.4e-39;
Matches 729; Conservative 0; Mismatches 477; Indels 3; Gaps 1;
QY 290 TTCAGATCATGCATCATCTCTCTGAGCATCCAAATGTTGTAGGATCAAGGACCTTATG 349
DB 1 TGCAGATCATGCATCATCTCTCTGAGCATCCAAATGTTGTAGGATCAAGGACCTTATG 60
QY 350 AAGATTCGGTGTGTTGTTTCAATATGTTATGAGGTTTGTGAAGTGTGAGCTTTTGTATC 409
DB 61 AGGACAAGCAGAGCGTGCACTCTGTCATGAGCTGTGCGGGCGGGGAGCTCTTCGACC 120
QY 410 GGATTTGTTTCTAAGGTCATTTTATGAGCGGTGAAGCTGTCAAGCTTTATTAAGCAATTC 469
DB 121 GCATCATCGCCGGGGGCGAGTACAGGAGCGCGCGCGGAGCTCTCGCGGCCATCG 180
QY 470 TTGGTGTGTTGAGCTGTGATCTCTTGTGTATGATGATGATGATGATGATGATGATGATG 529
DB 181 TGCAGATCGTGACACCTGCCACCTCCATCGGGGGGTGATGACCGGGGATCAAGCCCGAGA 240
QY 530 ATTCTCTGTTTATAGTCTCTAAGATGATGCTAAGCTTAAGCTTAAGCTTAAGCTTAAGCTT 589
DB 241 ACTTCTGCTGCTCAGCAGGAGGAGGAGCGCGCGCTCAAGCCACCGACTTCGGGCTCT 300
QY 590 CTGCTCTTCTAAGCCAGGACAAATATTTATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 649
DB 301 CGGCTCTTCTAAGGAGGGGAGCTGCTCAGGAGCATGCTCGGAGCGGCTTACTACATCG 360
QY 650 CACCAGAGGTCTAAGAAATGTTTATGAGCTGAATGATGTTGAGTGTGAGTGTGAGTGTGAGT 709
DB 361 CGCCCGAGGTGCTCAGAGAGAGTACGCGCGGAGCGGAGCATCTGGAGCGTCTCGGCTCA 420

QY 710 TCCTCTACATTTTACTCAGCGGTGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 769
DB 421 TGCTCTACATCT 480
QY 770 TTAGACAGATATTGCAAGGGAAGTTAGATTTCAAATCTGACCCCTGACCCCTGACCCCTGAC 829
DB 481 TCACCGCCATCTCTGAGGGCAGCTTGACCTCTCCAGGAGCCATGCGCACATCTCTCGC 540
QY 830 AAGCTCTAAAGATTGATCTATAAATGCTCGAAGAGAGCCCAAGAGAGGCAATTTCTG 889
DB 541 CGGAGCCCAAGATCTCTGTCAGAAAGATGCTCAACATCAACCCCAAGAGGCGCTCAGG 600
QY 890 CTCTAAGCCCTTGTCTCACCCTGATTCAGCCATGATTCAGAAAGAGAGAGAGAGAGAGAG 949
DB 601 CGTTCAGGTCTCTCAATCAACCCATGATCAAAAGAGAGAGAGAGAGAGAGAGAGAGAG 660
QY 950 TTGATCCAGAGCTTTATCT 1009
DB 661 TTGACAAACGTTGTTCTCGACAGGCTCAAGCAGGTTTCAGGGCCATGAACCCGTTCAAGAA 720
QY 1010 TGGCATTACGGGTAAATTGCTGAGAGACTTTCAGAGGAAAGAAATTTGGAGGTCTGAAGGA 1069
DB 721 CAGCATTGAGGATCATAGCTGGGTGCTTATCGAAGAGAGATCAAGGGCTGAAGGAGA 780
QY 1070 TGTTCAAGATGATAGACACAGCAACAGCGGAAAGATTTCTTTGAAGAGCTCAAGCGG 1129
DB 781 TGTTCAAGAACATTTGCAAGGATAACAGCGGAGCCATTTACCTCGACGAGCTCAACACG 840
QY 1130 GTTTGAAGAGAGTCGGATCTGAACCTGATGGAATCAGAAATCAAGTCTCTCTATGGATGCG 1189
DB 841 GGTGGCAAGACAGCGGCCCAAGCTGTCAAGCAGCGAAATGGAGAACTAATGGAAGCAG 900
QY 1190 CTGATATCGACAAACAGTGTGTA CAATAGACTACGGAAGATTTCTTAGCAGCAACCTTACACA 1249
DB 901 CTGACGCTGACGCAACGGGTTAAATGACTACGAGCAATTCGTACCGCAACAGTGCATA 960
QY 1310 GAAGCGGTTATATCACCATCGATGAGCTTCAGTCTGAGCTTTCAGTCTGAGAGTTTGGTCTAT 1369
DB 1021 ACAGCGGTACATTTACTTAAAGAGAGAGCTTGAGCAGCTTGAAGGAGCAAGGGTTGTATG 1080
QY 1370 ATACACCT---CTGGAGCAGCATGATCAAGGAGATTCATCTTGACAAATGACGGAAGATCG 1426
DB 1081 ACAGCGATAAAATCAAGAGACATCATCTCCGATGCCGACTCTGACAAATGATGGAAGATAG 1140
QY 1427 ATTTCTCGAGTTTACAGCAATGATGAGGAAAGGAGATGAGTTGGGAGAAAGCAAGAACCA 1486
DB 1141 ATTATTACAGATTTTGTGGCGATGATGAGGAAAGGAGCGGCTGTTGCCGAGCAATGAACA 1200
QY 1487 TGATGAAGA 1495
DB 1201 TCAAGAAGA 1209

RESULT 4
US-08-459-504B-20
; Sequence 20, Application US/08459504B
; Patent No. 6075185
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.

APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttle, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESS: No. 607518artis Corporation
STREET: 3054 Cornwalis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,504B
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/459,595
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CG1577/CIP/DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 1349 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHEetical: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 3..1226
OTHER INFORMATION: /note= "cDNA sequence for maize
pollen-specific calcium dependent protein kinase gene as
disclosed in Figure 30."
US-08-459-504B-20

Query Match 24.8%; Score 429.8; DB 3; Length 1349;
Best Local Similarity 60.3%; Pred. No. 1.4e-99;
Matches 729; Conservative 0; Mismatches 477; Indels 3; Gaps 1;
290 TTCAGATCATGCATCATCTCTCTGAGCATCCAAATGTTGTAGGATCAAAGGACTTATG 349
1 TGCAGATCATGCACCACTCTCGGGCAGCCCAACGTGTGGCCCTCCGGGGGTACG 60
350 AAGATTCGGTGTGTTGTTTCAATTTGTTATGAGGTTTGTGAAGGTGTGAGCTTTTGTATC 409
61 AGGCAAGCAGAGGTCACCTCTCTCATGAGCTGTGGCGGGGGGAGCTCTTCGACC 120
410 GGATGTTTCTAAGGTCATTTAGTGAAGCTGAAGCTGTCAAGCTTATTAAGACGATTC 469
121 GCATCATGCCCGGGGGGAGTACACGAGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 180
470 TTGGTGTGTTGAGGCTTGTCATCTCTTGGTGTGTTATGATAGAGATCTCAAACTTGAGA 529

DB 181 TGCAGATCGTGCACACCTGCCACTCCATGGGGGTGTATGACCCGGGACATCAAGCCCGAGA 240
QY 530 ATTTCTTCTTTGATAGTCTTAAGATGATCTAAGCTTAAGGCTAACGATTTTGGTTTGT 589
DB 241 ACTTCTGCTGCTCAGCAAGACGAGGACGGCGCTCAAGGCCACCGACTTCGGCTCT 300
QY 590 CTGCTTCTTAAGCCAGGACAAATTTATATGAGCTAGTTGAAGTCCGTACTATGTTG 649
DB 301 CGGTCTTCTCAAGGAGGGGAGTGTCTCAGGGACATCGTCGCGAGCGGCTACTCATCG 360
QY 650 CACCAAGGTGCTAAAGAAATGTTATGAGCTCAAAATAGATGTGTGAGTGTCTGTTGTTA 709
DB 361 CGCCGAGGTGCTCAAGAGGAGTACGGCCGGAGGCGCACTCGAGCGTGGGCTCA 420
QY 710 TCTCTACATTTTACTCAGCGGTGTTCTCTCTCTCTGGGAGAGACTGAGTCTGGAATCT 769
DB 421 TGCTCTACATCTTCTCTCGCGCGCTCTCTCTCTGGCAGAGAACGAGACGGCATCT 480
QY 770 TTAGACAGATATTGCAAGGGAAGTTAGATTTCAAAATCTGACCGTGGCTTACTATCTCAG 829
DB 481 TCACCGCATCTCTGGAGGGGAGCTTGACCTCTCCAGGAGCCATGGCCACACATCTCG 540
QY 830 AAGCTGCTAAAGATTGATCTATAAAATGCTCGAAAGAGCGCCCAAGAAACGCAATTTCTG 889
DB 541 CGGGAGCCAAAGGATCTCGTCAAGAAGATGCTCAACATCAACCCCAAGGAGCGCTCACGG 600
QY 890 CTCATGAAGCTTGTGTCAACCCATGATGTCGATGAACAGACAGCAGCAGCAAGGCTC 949
DB 601 CGTTCAGGTCTCTCAATCACCCATGATCAAGAGAGCGGAGACGCGCTTGACACGCGC 660
QY 950 TTGATCCAGCAGTCTTATCTCTCTTAAAGCAGTTTCTCAAAATGAATAAGATTAAAGAAA 1009
DB 661 TTGACAAACGTTGTTCTCGACAGGCTCAAGCAGTTTCAAGGCGCATGAACAGTTCAAGAAAG 720
QY 1010 TGGCATTACGGTAATTCCTGAGAGACTTTCAAGAGGAGAAATTTGGAGTCTGAAGGAT 1069
DB 721 CAGCATTTAGGATCATAGCTGGTCCCTATCCGAAGAGGAGATCAGAGGCTGAAGGAGA 780
QY 1070 TGTTCAGATGATAGACACAGCAACAGCGGAACGATTACTTTTGAAGAGCTCAAGCGG 1129
DB 781 TGTTCAGAAACATTGCAAGGATTAACAGCGGACCATTTACCTCGAGGCTCAACACAG 840
QY 1130 GTTTGAAGAGAGTGGATCTGAATCTGATGGAATCAGAAATCAAGTCTCTCATGATCGG 1189
DB 841 GGTTCGCAAGCAGCGGCGCCCAAGCTGTCAAGCAGCGAAATCGAGAAACTAATGAAGCAG 900
QY 1190 CTGATATCGACAACAGTGTGTACAATAGACTACGGAGAAATTCCTAGCAGCAACCTTACACA 1249
DB 901 CTGACGCTGACCGCAACGGTTAATTTGACTACGAGATTCGTCAACCGCAACAGTGATA 960
QY 1250 TGAACAAGATGAGAGAGAGGAGATCTGGTGGCTGCAATTTTCGAGCTTTGACAAAGACG 1309
DB 961 TGAACAAACTGGATAGAGAAGACACCTTTACACAGCATTCAGTATTTTCGACAAAGGACA 1020
QY 1310 GRAGCGTATATATCACCATCGATGAGTTCAGTCAAGTTCAGCAGAGTTTGGTCTATGTCG 1369
DB 1021 ACAGCGGTGACATTTACTAAGAGAGCTTTGACGCGCTTGAAGGAGCAAGGTTGTATG 1080
QY 1370 ATACACT---CTGGACGACATGATCAAGGAGATTTGATCTTGAACAATCAGCGGAGATCG 1426
DB 1081 ACGCCGATAAATCAAAGACATCATCTCCGATGCCGCTCTGACAAATGATGGAAGGATAG 1140
QY 1427 ATTTCTCGGAGTTTACAGCAATGATCAGGAAGGAGATGGAGTTGGGAGAGACGAAACA 1486
DB 1141 ATTATTCAGAGTTTGTGGCGATGATGAGAAAGGACCGCTGGTCCGAGCCATGAACA 1200
QY 1487 TGATGAAGA 1495
DB 1201 TCAGAAGA 1209

RESULT 5

US-08-459-444-20
Sequence 0, Application US/08459444A
Parent No. 6121014
GENERAL INFORMATION:

APPLICANT: Koziel, Michael G.
Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Lauris, Karen L.

TITLE OF INVENTION: METHOD FOR PRODUCING A PLANT-OPTIMIZED
NUCLEIC ACID CODING SEQUENCE

NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6121014artis Agribusiness Biotechnology Research, Inc.
STREET: 1054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/459,444A
FILING DATE: 02-Jun-1995
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION DATE: US 07/772,027
FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-18805/Pl/CGC1577/CIP/DIV6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8597
TELEFAX: (919)541-8689

INFORMATION FOR SEQ ID NO: /note= "cdna sequence for maize
pollen-specific calcium dependent protein kinase gene as
disclosed in Figure 30."

SEQUENCE CHARACTERISTICS:
LENGTH: 1349 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: linear
HYPOTHETICAL: NO
FEATURE:

NAME/KEY: CDS
LOCATION: 3..1226

SEQUENCE DESCRIPTION: SEQ ID NO: 20:

US-08-459-444-20

Query Match 24.6%; Score 429.8; DB 3; Length 1349;
Best Local Similarity 60.3%; Pred. No. 1.4e-99;
Matches 729; Conservative 0; Mismatches 477; Indels 3; Gaps 1;

QY 250 TTCAGATCATGATCTCTCTGAGCATCCAAATGTTGTTAGGATCAAGGGAGTTATG 349
DB 1 TGCAGATCATGACCACTCTCCGGCCAGCCCAACGTGGTGGCCCTCCGGCGCGGTACG 60

QY 350 AAGATTGGTGTGTTTCATATTGTTATGGAGTTGTGAAGTGGTGGTGTGTTGATC 409
DB 61 AGGCAAGCAGAGCGTGCACCTCTGTCATGGAGCTGTGCCGGCGGGAGGCTCTTCGACC 120

QY 410 GGATTGTTTCTAAGGTCATTTTAGTGAGCGTGAAGCTGTCAAGCTTATTAAAGAGTTC 469
DB 121 GCATCATCGCCCGGCGGCGAGTACACGAGCGCGCGCGGAGCTGCTGCGCGCATCG 180
QY 470 TTGGTGTGTTGAGGCTTGTCATTCCTTTGGTGTGTTATGCATAGAGATCTCAAACTGAGA 529
DB 181 TGCAGATCGTGCACACCTGCTCCATCGGGGTGATGACCCGGGACATCAAGCCCGAGA 240
QY 530 ATTCTTCTGTTGATAGTCTTAAAGATGATGCTAAAGCTAAAGCTACCGATTTTGGTTGT 589
DB 241 ACTTCTGCTGCTCAGCAAGGACGAGGACGCGCCCTCAAGGCCACCGACTTCGGCTCT 300
QY 590 CTGTCTCTATAAGCCAGACACATATTTATAGAGTGTGTTGGAGTCCGTACATATGTTG 649
DB 301 CCGTCTTCTTCAAGGAGGCGAGCTGCTCAGGAGACATGCTCGGAGCGCCTACTACATCG 360
QY 650 CACCAGAGGTGCTAAAGAAATGTTATGGACCTGAAATAGATGTTGGAGTCTGTTGTTA 709
DB 361 CGCCGAGGTGCTCAGAGGAGTACGCGCCCGAGGCGGACATCTGGAGCGCTCGGCCTCA 420
QY 710 TCCTCTACATTTTACTCAGCGGTGTTCTTCCCTTCTGGGCGAGAGCTGAGTCTGGAATCT 769
DB 421 TGCTCTACATCTTCTCGCGGCGTGCCTTCCCTTCTGGGCGAGAGAACCGGCATCT 480
QY 770 TTAGACAGATATTGCAAGGGAAGTTAGATTTCAAAATCTGACCCGTGGCTTACTATCTCAG 829
DB 481 TCACGGCATCTCTGGAGGCGAGCTTGACCTCTCCAGCGAGCGCATGGCCACACATCTCGC 540
QY 830 AAGTGTCTAAAGATTTGATCTATAAATGCTCGAAGAGAGCCCGAAGAAAGCATTTCTG 889
DB 541 CGGAGGCAAGGATCTCGTCAAGAGATGCTCAACATCAACCCCAAGGAGCGGTCTCAGG 600
QY 890 CTCATGAAGCCTTGTGTCAACCATGATGATGATGATGATGATGATGATGATGATGATG 949
DB 601 CGTTCAGGTCTCTCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 660
QY 950 TTGATCAGCAGCTTCTATCTGCTTAAAGCAGTTTCTCAATGATGATGATGATGATGATG 1009
DB 661 TTGCAACAGTGTGTTCTCGACAGCTCAAGCAGTTCAGGGCCATGAACAGTTCGAAGAA 720
QY 1010 TGGCATTCAGGTAATTTGCTGAGAGACTTTCAGAGAGAGAAATTTGAGGCTCTGAAGGA 1069
DB 721 CAGCATTTGAGGATCATAGCTGGGTGCTTATCGAAGAGAGAGATCAACAGGCTGAAGAGA 780
QY 1070 TGTTCAGATGATAGACACAGACAGCGGAGAGATTTTTCAGAGAGCTCAAGCGG 1129
DB 781 TGTTCAGAAACATTGACAGAGATAACAGCGGAGCATTACCCCTCAGCAGCTCAACACG 840
QY 1130 GTTTGAAGAGAGTCTGGATCTGAACTGATGGAATCAAGATCAAGATCAAGTCTCTCATGG 1189
DB 841 GGTTCGCAAGACAGCGGCCCAAGCTGTGACAGCAGGAAATGAGAGAACTAATGGAAGCAG 900
QY 1190 CTGATATCGCAACAGTGTGTACATAGACTAGCGGAGATTTCTAGCAGCAGCACTTACACA 1249
DB 901 CTGACGCTGACGCAACGGTTAAATGACTAGCAGAAATTCGTACCCGCAACAGTGCATA 960
QY 1250 TGAACAAGATGGAGAGAGAGGATTTCTGCTGGCTGCAATTTTCGGACTTTGACAAAGACG 1309
DB 961 TGAACAACCTGGATAGAGAGAGACCTTTACACAGCATTTCCAGTATTTTCGACAAAGACA 1020
QY 1310 GAAGGGTTATATCACCATCGATGAGCTTCACTCAGCTTGCACAGATTTTGGTCTATGTC 1369
DB 1021 ACAGCGGTATCTTACTTAAAGAGAGCTTGACAGCGCTTTGAAGGAGCAAGGTTGTATG 1080
QY 1370 ATACACCT---CTGGACGACATGATCAAGGAGATTTGATCTTGACAAATGACGGGAGATCG 1426
DB 1081 ACGCCGATAAATCAAAAGACATCATCTCCGATGCCGACTCTGACAAATGATGAAGATAG 1140
QY 1427 ATTTCTCGGATTTACAGCAATGATGAGGAGAGATGAGTGTGGGAGAGCAGCAACCA 1486
DB 1141 ATTATTCAGAGTTTGTGGCGATGATGAGGAAAGGACGCTGGTCCGCGCAATGAAACA 1200
QY 1487 TGAAGAAGA 1495

Db 1081 ACGCGGATAAAATCAAGACATCATCTCCGATGCCGACTGTGACAAATGATGGAAGGATAG 1140
QY 1427 ATTCTCGAGTTTACAGCATGATGAGGAAGGAGATGGAGTTGGAGAAGCAGAACCA 1486
Db 1141 ATTATTCAGAGTTTGTGGCGATGATGAGGAAGGAGCGGTGTGGCGGACCAATGAACA 1200
QY 1487 TGATGAAGA 1495
Db 1201 TCAAGAAGA 1209

RESULT 7
US-08-459-448A-26
; Sequence 26, Application US/08459448A
; Patent No. 5859336
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5859336attis Corporation
; STREET: Patent & Trademark Dept., 520 White Plains
; STREET: Rd. POB 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,448A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Gary M.
; REGISTRATION NUMBER: 40403
; REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8582
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4162 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO

FEATURE:
NAME/KEY: misc.feature
LOCATION: 1418..1427
OTHER INFORMATION: /note= "start of mRNA".
FEATURE:
NAME/KEY: exon
LOCATION: 1481..2366
FEATURE:
NAME/KEY: intron
LOCATION: 2367..2451
FEATURE:
NAME/KEY: exon
LOCATION: 2452..2602
FEATURE:
NAME/KEY: intron
LOCATION: 2603..2690
FEATURE:
NAME/KEY: exon
LOCATION: 2691..2804
FEATURE:
NAME/KEY: intron
LOCATION: 2805..2906
FEATURE:
NAME/KEY: exon
LOCATION: 2907..3075
FEATURE:
NAME/KEY: intron
LOCATION: 3076..3177
FEATURE:
NAME/KEY: exon
LOCATION: 3178..3304
FEATURE:
NAME/KEY: intron
LOCATION: 3305..3398
FEATURE:
NAME/KEY: exon
LOCATION: 3399..3498
FEATURE:
NAME/KEY: intron
LOCATION: 3499..3713
FEATURE:
NAME/KEY: exon
LOCATION: 3714..3811
FEATURE:
NAME/KEY: promoter
LOCATION: 1..1477
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /partial
OTHER INFORMATION: /function= "pollen-specific promoter region"
OTHER INFORMATION: /evidence= EXPERIMENTAL
US-08-459-448A-26
Query Match 12.5%; Score 218; DB 2; Length 4162;
Best Local Similarity 59.8%; Pred. No. 9.4e-46;
Matches 365; Conservative 0; Mismatches 245; Indels 0; Gaps 0;
QY 142 TACCITCTGGGAAAAGCTAGGCCAAGCCAAATTGGAAACAACCTATCTCTGCACAGAG 201
Db 1757 TACTCATGGCAAGAGCTCGGCGCGGCGGAGTTCGCGTGACGACCTGTGCACGAC 1816
QY 202 AAATCAACCTCCGCTAATTACGCCCTGCAAAATCGATCCGGAAGCGAAAGCTCGTGTGCG 261
Db 1817 CGGACGAGCGGCGGAGAGCTGGCTGCAAGACGATCGGGAAGCGGAAGCTCGCGCCAGG 1876
QY 262 GAGGATTAGAGATGATGGCGTGAGATTCAGATCATGATCATCTCTGAGCATCCA 321
Db 1877 GAGGAGTGGAGACGTCGGCGGGAGGTGCAGATCATGCACCTCTCCGCGCAGCCC 1936
QY 322 AATGTTGTTAGGATCAAGGGGACTTATGAAGATTGCGTGTGTTGTTTCATATTGTTATGGAG 381
Db 1937 AACGTGTTGGGCTCCGCGCGCGTACGAGGACAAGAGCGGTGCACCTCGTCATGGAG 1996
QY 382 GTTTGTGAAGGTGGTGAAGCTTTTGTGATCGGATTGTTTCTAAAGGTCAATTTAGTGAGCGT 441

Db 1997 CTGTGCGCGGCGGAGCTCTTCGACCGCATCATCCCGGGCCGAGTACACGGAGCGC 2056
Qy 442 GAAGCTGTCAAGCTTATTAAAGACCATCTTGGTGTGTTGAGGCTTGTCTATCTCTTTGCT 501
Db 2057 GCGCGCGGAGCTGCTGGCGGCATCGTCAGATCGTCACACCTGCCACTCCATGGGG 2116
Qy 502 GTTATGATAGAGATCTCAACCTGAGAAATTTGTTGATAGTCTTAAGATGATGCT 561
Db 2117 GTGATGACCGGCGCATCAACCGCGAAGCTTCTGCTGCTCAGCAAGGACGAGGACGGC 2176
Qy 562 AAGCTTAAGGTACCGATTGTTGGTGTGTTCTTCTATAAGCCAGACATAATTTATAT 621
Db 2177 CCGCTCAAGGCCACCGACTTCGGCTCTCCGCTCTTCTCAAGNGGCGAGCTGCTCAGG 2236
Qy 622 GACGTAGTTGAAGTCCGATCTGTTGACCCAGAGTGCTTAAGAAATTTATGACCT 681
Db 2237 GACATCGTCGCGAGCGCTACTACATCGCGCCGAGGTGCTCAAGAGGAAGTACGCGCCG 2296
Qy 682 GAAATAGATGTGGAGTGGTGTGTTATCTCTACATTTTACTCAGCGGTGTTCTCTCC 741
Db 2297 GAGCGCGACATCTGGAGCTGCGGCTGATGCTCTACATCTTCTCGCGCGCTGCTCTCC 2356
Qy 742 TTCTGGGCGAG 751
Db 2357 TTCTGGGCGAG 2366

RESULT 8

US-08-459-595A-26
; Sequence 26, Application US/08459595A
; Patent No. 6018104
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Warren, Vance C.
; APPLICANT: Krammer, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6018104artis Corporation
; STREET: Patent & Trademark Dept., 520 White Plains
; STREET: Rd., POB 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,595A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: 40403
REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8582
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 4162 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: misc feature
LOCATION: 1418..1427
OTHER INFORMATION: /note= "start of mRNA"
FEATURE:
NAME/KEY: exon
LOCATION: 1481..2366
FEATURE:
NAME/KEY: intron
LOCATION: 2367..2451
FEATURE:
NAME/KEY: exon
LOCATION: 2452..2602
FEATURE:
NAME/KEY: intron
LOCATION: 2603..2690
FEATURE:
NAME/KEY: exon
LOCATION: 2691..2804
FEATURE:
NAME/KEY: intron
LOCATION: 2805..2906
FEATURE:
NAME/KEY: exon
LOCATION: 2907..3075
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NAME/KEY: intron
LOCATION: 3076..3177
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NAME/KEY: exon
LOCATION: 3178..3304
FEATURE:
NAME/KEY: intron
LOCATION: 3305..3398
FEATURE:
NAME/KEY: exon
LOCATION: 3399..3498
FEATURE:
NAME/KEY: intron
LOCATION: 3499..3713
FEATURE:
NAME/KEY: exon
LOCATION: 3714..3811
FEATURE:
NAME/KEY: promoter
LOCATION: 1..1477
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /partial
OTHER INFORMATION: /function= "pollen-specific promoter region"
OTHER INFORMATION: /evidence= EXPERIMENTAL
US-08-459-595A-26

Query Match 12.5%; Score 218; DB 3; Length 4162;
Best Local Similarity 59.8%; Pred. No. 9.4e-46;
Matches 365; Conservative 0; Mismatches 245; Indels 0; Gaps 0;

Qy 142 TACCTTCTGGGAAAAAGCTAGCCAGGCAATTTGGACAACTATCTCTGCACAG 201
Db 1757 TACTCGATGGCAAGGAGCTCGGCGCGGCGAGTCTGGCGGTGACGACCTGTGCGACGCAC 1816
Qy 202 AAATCAACCTCCGCTAATTACGCTCGCAATCGATCCGGAAGCGAAAGCTCGTGTGTGCGC 261
Db 1817 CGGACGAGCGCGAGAGCTGGCGTCAAGACGATCCGGAAGCGAAAGCTCGGCGCGCAGG 1876
Qy 262 GAGGATTACGAAGATGTATGTCGCTGAGATTGAGATCATGTCATCATCTCTCTGAGCATCCA 321
Db 1877 GAGGACGTGGACGAGCTGCGCGCGGCGAGTGCAGATCATGACCACTCTCTCGGCGCAGCC 1936
Qy 322 AATGTTGTAGATCAAGGACATTAAGAGATTCGCTGTTTGTATATGTTATGAGG 381
Db 1937 AACGTGGTGGGCGCTCGGCGCGCGGTACGAGCAAGCAGAGCGTGACCTCGTCATGGAG 1996
Qy 382 GTTGTGAAGTGTGAGCTTTTGTATGCGATTTCTTAAAGTCAATTTTATGAGCGT 441
Db 1997 CTGTGCGCGCGCGGAGCTCTTCGACCGCATCATCGCCGGGCGCAGTACAGGAGCGC 2056
Qy 442 GAAGCTGTCAAGCTTATTAAAGACATTCCTGCTGTTGAGGCTTGTGCTTCTTCTTGGT 501
Db 2057 GCGCGCGCGGAGCTCTCGCGCGCATCTGCGACATCTGCTGCTCAGCAAGGAGGAGCGCG 2176
Qy 502 GTTATGCTAGAGATCTCAAACTCAGAAATTTCTTTTGTATGTCCTTAAAGATGATGCT 561
Db 2117 GTGATGCGCGCGGACATCAAGCCCGGAGACTTCTGCTGCTCAGCAAGGAGGAGCGCG 2176
Qy 562 AAGCTTAAGCTTACGATTTGCTGTTGCTGCTCTCTATAGCCAGGACATATTATAT 621
Db 2177 CCGCTCAAGCCAGCGAGCTCTCGCGCTCTCGCTCTCTTCTTCAAGGAGGCGAGCTGCTCAGG 2236
Qy 622 GACGTAGTTGGAAGTCCGCTACTATGCTGACCAAGAGTGTAAAGAAATGTTATGAGCT 681
Db 2237 GACATCTCGGAGCGGCTACTACTACGCGCGCGAGTGTCTCAAGAGGAGTACGCGCGC 2296
Qy 682 GAAATAGATGTGGAAGTCTCGGTGTTATCTCTACATTTTACTCAGCGGTGTTCTTCCC 741
Db 2297 GAGGCGGACATCTGAGAGCTCGCGCTCTGCTCTACTCTTCTCGCGCGGCGCTGCTCCC 2356
Qy 742 TTCTGGGCGAG 751
Db 2357 TTCTGGGCGAG 2366

RESULT 9

US-08-459-504B-26

Sequence 26 Application US/08459504B

Patent No. 6075185

GENERAL INFORMATION:

APPLICANT: Koziel, Michael G.
APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlino, Ellis J.
APPLICANT: Launis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttle, Janet L.

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED

TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 6075185artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park

STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,504B
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/459,595
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC1577/CIP/DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8887
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 4162 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: misc feature
LOCATION: 1418..1427
OTHER INFORMATION: /note= "start of mRNA"
FEATURE:
NAME/KEY: exon
LOCATION: 1481..2366
FEATURE:
NAME/KEY: intron
LOCATION: 2367..2451
FEATURE:
NAME/KEY: exon
LOCATION: 2452..2602
FEATURE:
NAME/KEY: intron
LOCATION: 2603..2690
FEATURE:
NAME/KEY: exon
LOCATION: 2691..2804
FEATURE:
NAME/KEY: intron
LOCATION: 2805..2906
FEATURE:
NAME/KEY: exon
LOCATION: 2907..3075
FEATURE:
NAME/KEY: intron
LOCATION: 3076..3177
FEATURE:
NAME/KEY: exon
LOCATION: 3178..3304
FEATURE:
NAME/KEY: intron
LOCATION: 3305..3398
FEATURE:
NAME/KEY: exon
LOCATION: 3399..3498
FEATURE:

NAME/KEY: intron
LOCATION: 3499..3713
FEATURE:
NAME/KEY: exon
LOCATION: 3714..3811
US-08-459-504B-26
Query Match 12.5%; Score 218; DB 3; Length 4162;
Best Local Similarity 59.8%; Pred. No. 9, 4e-46;
Matches 365; Conservative 0; Mismatches 245; Indels 0; Gaps 0;
QY 142 TACCTTCTGGAAAAAGCTGAGCCAAAGCCAAATTTGGAAACAACTATCTCTGCACAGAG 201
DB 1757 TACTCGATGGCGAAGAGCTGCGCGCGGCGAGTTCGGGCTGACGACCTGTGACGCGAC 1816
QY 202 AAATCAACCTCCGCTAATTAACGCTCCGAATCGATCCGAAAGCGAAAGCTGTGTGCGC 261
DB 1817 CGGACGAGCGCGGAGAGCTGGCGTCCAGACGATCGGAAAGCGGAGCTGGCGCCAGG 1876
QY 262 GAGGATTACGAAGATGTATGGCTGAGATTTCAGATCATCATCTCTCTGAGCATCCA 321
DB 1877 GAGGACGTGACGAGCTGCGCGGGAGGTGCAGATCATGCACACCTCTCCGCGCAGGCC 1936
QY 322 AATGTTTATAGGATCAAGGACCTTATGAGATTCGGTGTGTTTCATATCTTTATGGAG 381
DB 1937 AACGTGTGGGCTCCGCGCGCTACGAGGACAGAGAGCTGCACTCTCTCATGTGAG 1996
QY 382 GTTGTGAAGTGTGTGAGCTTTTGTATCGGATTTTCTTAAAGGTCAITTTAGTGAGCGT 441
DB 1997 CTGTGCGCGGGGGAGCTCTTCGACCGCATCATCGCCGGGCGAGTACACGAGCGC 2056
QY 442 GAAGCTGTCAAGCTTATTAAGAGCATCTTGTGTTGTTGAGGCTGTGCACTCTCTTGT 501
DB 2057 GGGCGCGGAGGTGTGCGCGCGCATCTGTCAGATCTGTCACACCTGCCACTCCATGGG 2116
QY 502 GTTATGATAGATCTCAAACTGAGATTCTTGTGTTGATGCTCTAAAGATGATGT 561
DB 2117 GTATGACCGGACATCAAGCCGAGACTTCTGCTGCTAGCAAGGACGAGACGG 2176
QY 562 AAGCTTAAGCTACCGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 621
DB 2177 CCGCTCAAGGCCACCGACTTCGGGCTCTCGTCTTCTTCAAGGAGGCGAGCTGCTCAGG 2236
QY 622 GACGCTTGGAGTCCGTAATGTTGTCACGAGAGTGTCTAAGAAATGTTATGACCT 681
DB 2237 GACATCTGCGGACGCGCTACTACATCGCCCGAGGTGCTCAAGAGGAAGTACGGCCG 2296
QY 682 GAAATAGATGTGTGAGTGTGTGTTTATCTCTACATTTTACTCAGCGTGTCTCTCC 741
DB 2297 GAGCGCGACATCTGAGCGTGGCGTCTATGCTCTACATCTTCTCGCGCGGTGCTCC 2356
QY 742 TTCTGGGCGAG 751
DB 2357 TTCTGGGCGAG 2366

RESULT 10
US-08-459-444-26
Sequence 26, Application US/08459444A
Patent No. 6121014
GENERAL INFORMATION:
APPLICANT: Kozziel, Michael G.
Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Launis, Karen L.
TITLE OF INVENTION: METHOD FOR PRODUCING A PLANT-OPTIMIZED
NUCLEIC ACID CODING SEQUENCE

NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6121014artis Agribusiness Biotechnology Research, Inc.
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,444A
FILING DATE: 02-Jun-1995
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/SOCKET NUMBER: S-18805/P1/CGC1577/CIP/DIV6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 4162 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: misc feature
LOCATION: 1418..1427
OTHER INFORMATION: /note= "start of mRNA"
FEATURE:
NAME/KEY: exon
LOCATION: 1481..2366
FEATURE:
NAME/KEY: intron
LOCATION: 2367..2451
FEATURE:
NAME/KEY: exon
LOCATION: 2452..2602
FEATURE:
NAME/KEY: intron
LOCATION: 2603..2690
FEATURE:
NAME/KEY: exon
LOCATION: 2691..2804
FEATURE:
NAME/KEY: intron
LOCATION: 2805..2906
FEATURE:
NAME/KEY: exon
LOCATION: 2907..3075
FEATURE:
NAME/KEY: intron
LOCATION: 3076..3177
FEATURE:
NAME/KEY: exon
LOCATION: 3178..3304
FEATURE:
NAME/KEY: intron
LOCATION: 3305..3398
FEATURE:
NAME/KEY: exon

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;
; LOCATION: 3399..3498
; FEATURE:
; NAME/KEY: intron
; LOCATION: 3499..3713
; FEATURE:
; NAME/KEY: exon
; LOCATION: 3714..3811
; SEQUENCE DESCRIPTION: SEQ ID NO: 26:
;
US-08-459-444-26

Query Match      12.5%  Score 218;  DB 3;  Length 4162;
Best Local Similarity 59.8%;  Pred. No. 9.4e-46;
Matches 365;  Conservative 0;  Mismatches 245;  Indels 0;  Gaps 0;

QY 142 TACCTTTGGGAAAAGACTAGGCAAGGCCAATTTGGAACAACCTATCTCTCCACAGAG 201
DB 1757 TACTCGATGGGCAAGGAGCTCGGGCGGGGAGTTCGGCGTGACGACCTGTGCGCCAC 1816
QY 202 AATCAACCTCGCTAATTACGCTCGAAATCGATCCGGAAGCGAAAGCTCGTGTGTCG 261
DB 1817 CGACGACGGGGAGAACTGGGTGCGAGATCGGAGCGGAAGCTGGCGGCCAGG 1876
QY 262 GAGGATTACGAGATGTAAGCGTGAGATTCAGATCATGATCATCTCTCTGAGCATCCA 321
DB 1877 GAGGACGTGGACACGTGCGGGGAGGTGAGATCATGACACCACTCTCTCGGCCAGCC 1936
QY 322 AATGTGTAGATCAAGAGGACTTATGAAGATTCGGTGTGTTGTCATATTGTTATGGAG 381
DB 1937 AACGTGGTGGGCTCCGGCGCGCGTACGAGGACAGCAGCGTGCACCTCTGTCATGGAG 1996
QY 382 GTTGTGAAGTGTGAGCTTTTGTATCGGATTTGTTCTAAAGTCTATTTTGTAGCGGT 441
DB 1997 CTGTGCGGGCGGGAGGCTCTTCACCGCATCATCGCCGGGCCAGTACACGGAGCGC 2056
QY 442 GAAGTGTCAACTTATTAGACGATTTCTGTTGTTGAGGCTTGTCTATCTCTCTGTT 501
DB 2057 GCGCGCGGAGCTGCTGCGGCCATCTGCGATCGGATCGTGACACTGCCACTCATGGGG 2116
QY 502 GTATGATAGATGATCTCAAACTGAGATTTCTTTGTTGATGCTCTTAAAGATGATGCT 561
DB 2117 GTATGACACCGGAGATCAAGCCGAGAACTCTCTGCTGCTCAGCAGGACGAGAGCGC 2176
QY 562 AAGCTTAAGCTACCGATTTGGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 621
DB 2177 CGCTCAAGGCCACCGACTTCGGCTCTCCGCTCTCTTCTTCAAGGAGGCGGAGCTCTCAGG 2236
QY 622 GACGTAGTTGGAAGTCCGACTATGTTGACAGAGGTGCTAAAGAAATGTTATGACCT 681
DB 2237 GACATGTCGGCAGCCCTACTACATCGCGGCCGAGGTGCTCAAGAGGAAGTACGGCCCG 2296
QY 682 GAAATAGATGTGTGAGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 741
DB 2297 GAGGCGGACATCTGGAGCGTGGGCTCTCATCTCTATCTCTATCTCTCTCTCTCTCT 2356
QY 742 TTCTGGGCGAG 751
DB 2357 TTCTGGGCGAG 2366

RESULT 11
US-09-547-422-26
; Sequence 26, Application US/09547422
; Patent No. 6320100
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
;            Desai, Nalini M.
;            Lewis, Kelly S.
;            Kramer, Vance C.
;            Warren, Gregory W.
;            Evola, Stephen V.
;            Crossland, Lyle D.
;            Wright, Martha S.
;            Merlin, Ellis J.
;

```

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;
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
;                     INSECTICIDAL ACTIVITY IN MAIZE
;
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESS: No. 6320100artis Agribusiness Biotechnology Research, Inc.
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/547,422
; APPLICATION NUMBER: US/09/547,422
; FILING DATE: 11-Apr-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/459,595
; FILING DATE: 02-JUN-1995
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: S-18805H
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8567
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4162 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1418..1427
; OTHER INFORMATION: /note= "start of mRNA"
;
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1481..2366
;
; FEATURE:
; NAME/KEY: intron
; LOCATION: 2367..2451
;
; FEATURE:
; NAME/KEY: exon
; LOCATION: 2452..2602
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; FEATURE:
; NAME/KEY: intron
; LOCATION: 2603..2690
;
; FEATURE:
; NAME/KEY: exon
; LOCATION: 2691..2804
;
; FEATURE:
; NAME/KEY: intron
; LOCATION: 2805..2906
;
; FEATURE:
; NAME/KEY: exon
; LOCATION: 2907..3075
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; FEATURE:
; NAME/KEY: intron
; LOCATION: 3076..3177
;
; FEATURE:
; NAME/KEY: exon
; LOCATION: 3178..3304
;

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RESULT 12
US-07-351-715A-26
; Sequence 26, Application US/07951715A
; Patent No. 5625136
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.

LOCATION: 2907..3074
FEATURE: intron
NAME/KEY: 3075..3177
LOCATION: 3075..3177
FEATURE: exon
NAME/KEY: 3178..3305
LOCATION: 3178..3305
FEATURE: intron
NAME/KEY: 3306..3397
LOCATION: 3306..3397
FEATURE: exon
NAME/KEY: 3398..3497
LOCATION: 3398..3497
FEATURE: intron
NAME/KEY: 3498..3712
LOCATION: 3498..3712
FEATURE: exon
NAME/KEY: 3713..3811
LOCATION: 3713..3811
US-07-951-715A-26

Query Match 12.5%; Score 218; DB 1; Length 4165;
Best Local Similarity 59.8%; Pred. No. 9.4e-46;
Matches 365; Conservative 0; Mismatches 245; Indels 0; Gaps 0;
QY 142 TACCTTCTGGAAAAAGCTAGCCAAAGCCAAATTTGGAACAAACCTATCTCTGCACACAG 201
Db 1755 TACTCGATGGCAAGAGCTCGGGCGGGCAGTTTCGGGTGACGCACCTGTGCACGCAC 1814
QY 202 AATCAACCTCCGCTAATTAAGCTGCAATCGATCCGAGCGAAGCTCGTGTGTCG 261
Db 1815 CGACGAGCGCGAGAAGCTGGCGTGCAGACGATCGGAAGCGGAAGCTGGCGCCACG 1874
QY 262 GAGGATTACAGAGATGATGGCTGAGATTGATCATCATCTCTCTGAGCATCCA 321
Db 1875 GAGACGTGACAGCTGGCGGGAGGTGCAATCAATGACACCTCTCCGGCCAGCC 1934
QY 322 AATGTTGTTAGGATCAAGAGACTTATAGAGATTCGTTGTTGTTGTTGTTGTTGTTG 381
Db 1935 AAGCTGTGGGCTCCGGCGCGGTACGAGGACAAAGCAGAGCGTGCACCTCGTCATGG 1994
QY 382 GTTGTGAAGGTGTGAGCTTTTGTGATCGATTGTTTCTAAAGGTCAATTTAGTGAGCGT 441
Db 1995 CTGTGCGGGCGGGAGCTCTTCGACCGATCATCGCCGGGGCCAGTACACGAGCGC 2054
QY 442 GAAGCTCTCAAGCTTAATTAAGACGATTTGTGTTGTTGTTGTTGTTGTTGTTGTTG 501
Db 2055 GGGCCCGGAGCTGTGCGGCCATCTGTGCAGATCGTGCACACCTGCCACCTCCATGGG 2114
QY 502 GTTATGATAGATCTCAACCTGAGATTTCTTGTGATAGTCTTAAAGATGATGCT 561
Db 2115 GTGATGACCGGGACATCAAGCCGAGAACTTCTGCTGCTCAGCAGCAGCAGCGG 2174
QY 562 AAGCTTAAGGCTACCGATTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 621
Db 2175 CGCTCAAGGCCACCGACTTCGGCTCTCCGCTCTCTTCAAGAGGGCGAGCTGCTCAG 2234
QY 622 GACGTAGTGAAGTCGCTACTAGTTGTCACGAGCTGCTCAAGAAATGTTATGACCT 681
Db 2235 GACATGTCGCGCGGCTACTACTCGCCCGAGGTGCTCAAGAGGAAGTACGGCCG 2294
QY 682 GAAATAGATGTGGAGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 741
Db 2295 GAGCGGACATCTGGAGCTGGCGGTGATGCTCTACATCTTCTCGCGCGGTGCTCC 2354
QY 742 TCTGGGCGAG 751
Db 2355 TTCTGGGCGAG 2364

RESULT 13
US-09-347-801-3
Sequence 3, Application US/09347801

Patent No. 6262345
GENERAL INFORMATION:
APPLICANT: Allen, Steve
APPLICANT: Lee, Jian Ming
TITLE OF INVENTION: Plant Protein Kinases
FILE REFERENCE: BB-1171
CURRENT APPLICATION NUMBER: US/09/347,801
CURRENT FILING DATE: 1999-07-02
EARLIER APPLICATION NUMBER: 60/092,438
EARLIER FILING DATE: July 10, 1998
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Microsoft Office 97
SEQ ID NO 3
LENGTH: 2374
TYPE: DNA
ORGANISM: Oryza sativa
US-09-347-801-3

Query Match 10.9%; Score 189.6; DB 4; Length 2374;
Best Local Similarity 53.8%; Pred. No. 1.2e-38;
Matches 440; Conservative 0; Mismatches 369; Indels 9; Gaps 2;
QY 271 GAAGATGATGGCGTGAGATTTCAGATCATCATCTCTCTGAGCATCCAAATGTTGT 330
Db 846 GAGGATGTTCTGAGAGTAAATTTTGAGAGCGTTATCAGGCGCAATAATCTCGTC 905
QY 331 AGGATCAAGGAGCTTATGAAGATTCGGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 390
Db 906 AATATCTATGATGATGTGAGGATGGCTCAATGTCATGTTGTCATGTTGTTGTTGTTGTTG 965
QY 391 GGCTGTGAGCTTTTGTGCGGATTGTTTCTAAAGGTCAATTTTGTAGTGCCTGAAGCTGTC 450
Db 966 GAGGAGAAATGCTAGACAGATATTAGCCAGAGCGGAGATACACAGAGGAAGATGCC 1025
QY 451 AA---GCTTATTAAAGCACTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 507
Db 1026 AAGCGATTGTTGATGAGATTTTGAGCGTAGTAGCTTCTGTCATCTTCAGGGGGTAGTG 1085
QY 508 CATAGATCTCAACCTCGAGATTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 567
Db 1086 CATCGTGAATTAAGCCAGAGAAATTTCTTTTCAACAGGAGTGAATGTTCTCCCATG 1145
QY 568 AAGGCTACCGATTTTGGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 627
Db 1146 AAGTTGATGATTTTGGTCTCTCTGATTTTATTAGCCAGATGAAGGCTTAATGATATT 1205
QY 628 GTTGAAGTCCGCTACTATGTTGACAGAGCTGCTTAAGAAATGTTATGAGACCTGAATA 687
Db 1206 GTTGAAGTGCATATATGTTGCCCCAGAGGTTTACAGATCATATAGTATGGAAGCA 1265
QY 688 GATGTGTGAGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 747
Db 1266 GACATTTGGAGTATAGTGTCTATACGTACATTTCTGCTCTGTCGAGTCGGCCATTCTGG 1325
QY 748 GCAGAGCTGAGTCTGGAATCTTTAGACAGATATTGCAAGGAGTATGAGATTTCAATCT 807
Db 1326 GCACGAACAGAAATCAAGAAATTTCCGATCTGTGTTGAGAGCTGATCCCACTTTGATGAT 1385
QY 808 GACCGTGGCCTACTATCTCAGAAGCTGCTAAAGATTTGATCTATAAATGCTCGAAAG 867
Db 1386 TCACCGTGGCTACATATACGTAGCTGAGCTAAGGATTTTGTGAAGAGATTTCTGAACAA 1445
QY 868 AGCCCCAAGAAACGCAATTTCTGCTCATGAAGCTTTGTTCACCCATGATTTGTCGATGAA 927
Db 1446 GATTACCGCAAAAGATGACCGCTGTTCAAGCACTGATCATCTTGGTTGGAGATGAA 1505
QY 928 CAAGCAGCACACAGAGCTCTTTGATCCAGCAGCTTATCTGCTCTAAAGCAGTCTTCT 987
Db 1506 CA-----AAGGAGATCCGCTGGACATCTCACTTCAGATTAATTAAGCAATACCTC 1559
QY 988 CAATGAATTAAGATTAAGAAATGCAATTAACCGGTAATTTGCTGAGAGACTTTTCAGAGAA 1047
Db 1560 CGCGCTACACCTCTCTAAAGGTTGGCATTAAAGGCACCTATCCAAAGGCTTTAAGGGAAGAT 1619

QY 1048 GAAATTCGAGCTCTGAGGAATTTGTTCAAGATCATAGA 1085
 DB 1620 GAACCTTTGATCTCAAACTGCAGTTTAACTCTCTGA 1657

RESULT 14

US-08-464-164-1
 ; Sequence 1, Application US/08464164
 ; Patent No. 5614195
 ; GENERAL INFORMATION:
 ; APPLICANT: Tomley, Fiona M.
 ; APPLICANT: Dunn, Paul P. J.
 ; APPLICANT: Bumstead, Janene M.
 ; APPLICANT: Vermeulen, Arno N.
 ; TITLE OF INVENTION: Coccidiosis poultry vaccine
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Akzo No. 5614195el Patent Department
 ; STREET: 1300 Piccard Drive, Suite 206
 ; CITY: Rockville
 ; STATE: Maryland
 ; COUNTRY: U.S.A.
 ; ZIP: 20850
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/464,164
 ; FILING DATE: June 2, 1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Gormley, Mary E.
 ; REGISTRATION NUMBER: 34,409
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (301) 258-5200
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1400 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; C-TERMINAL
 ; FRAGMENT TYPE:
 ; ORIGINAL SOURCE:
 ; ORGANISM: Eimeria maxima
 ; STRAIN: Houghton
 ; DEVELOPMENTAL STAGE: sporozoite
 ; IMMEDIATE SOURCE:
 ; LIBRARY: sporozoite cDNA cloned in Lambda ZAPII
 ; CLONE: Em70-1
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 1..1368
 ; US-08-464-164-1

Query Match 9.4%; Score 165; DB 1; Length 1400;
 Best Local Similarity 54.5%; Pred. No. 1.6e-32;
 Matches 330; Conservative 0; Mismatches 275; Indels 0; Gaps 0;

QY 313 GAGCATCCAAATGTTGTTAGGATCAAGGGACTTATGAGATTCGGTGTGTTGTTCAATT 372
 DB 151 GATCATCTTAATCATGAATATATGAAATCTTTGAGGATAAAGGATCTTTTATCTT 210
 QY 373 GTTATGGAGTTGTGAAGGTGGTGGCTTTTGTGTCGATGTTTCTTAAGGTCATTT 432
 DB 211 GTTACAGAAGTATACAGGAGGAGAAATTTATGTAAGAAATTAATTAATCGAAAAAGATTC 270
 QY 433 AGTGAGCGTGAAGTGTCAAGCTTTATTAAGACGATTTGTTGTTGTGAGCTTGTGAT 492

DB 271 AGCAGGCGGATGCGAGCTCGTATAGTACGTCAAGTTCTATCGGGTATAAATTTATATGCA 330
 QY 493 TCTCTTGGTGTATGATAGATCTCAAACTGAGAAATTTCTTGTGTTGATAGTCTCTAAA 552
 DB 331 CGTAATAAAATAGTTCATAGAGATTTAAAGCCAGAGATTTATTTATAGAGATAAAAA 390
 QY 553 GATGATGCTAAGCTTAAAGCTACCGATTTTGGTTTGTCTGTCTCTATAGCCAGGACAA 612
 DB 391 AAAGATGCAAAATATACGAATTTATGTTTGGTTTATCTACACATTTTGGAGCCCAAAA 450
 QY 613 TATTATATGACGTAGTTCGTAAGTCCGTACTATGTTGCACACAGAGTCTCTAAAGAAATGT 672
 DB 451 AAATGAAGATAAATTCGGACCGGTACTACATTTGCCCTGAGGTCTGCACGGAACA 510
 QY 673 TATGGACCTGAAATAGATGTGGAGTGTGTGTATTCCTCTACATTTTACTCAGCGGT 732
 DB 511 TAGCATGAGAAATCGACGCTCTGGTCTACGGGTGTTATCTCTATATCTCTCTCTCGT 570
 QY 733 GTTCCTCCCTCTGGGCAGAGACTGAGTCTGGAATCTTTAGACAGATATTGCAAGGGAAG 792
 DB 571 TGTCCTCCATTTAACGGAGCAATGAAATTTGAAATCTTAAGAAAGTCGAGAAAGAAAA 630
 QY 793 TTAGATTTCAAATCTGACCCGTGGCTACTATCTCAGAAAGTGTCTAAAGATTTGATCTAT 852
 DB 631 TTCACCTTGGATTTACACAGTGGCGTAAAGTTAGCGAGCCAGCAAAAGATTTAATTAGG 690
 QY 853 ABAATGCTGAAAGGAGCCCAAGAACCATTTCTGTCATGAGCCCTTGTGTCCACCCA 912
 DB 691 AAGATGTTAGCATATGTACCCCTCAATGCGTATATCAGCAAAAGATGATATGATCATCA 750
 QY 913 TGGAT 917
 DB 751 TGGAT 755

RESULT 15

US-08-338-057-1
 ; Sequence 1, Application US/08338057
 ; Patent No. 5795741
 ; GENERAL INFORMATION:
 ; APPLICANT: Tomley, Fiona M.
 ; APPLICANT: Dunn, Paul P. J.
 ; APPLICANT: Bumstead, Janene M.
 ; APPLICANT: Vermeulen, Arno N.
 ; TITLE OF INVENTION: Coccidiosis poultry vaccine
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Organon Teknika Corporation
 ; STREET: 1330 Piccard Drive
 ; CITY: Rockville
 ; STATE: Maryland
 ; COUNTRY: U.S.A.
 ; ZIP: 20850
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/338,057
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: EP 93.309078.9
 ; FILING DATE: 12-NOV-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Gormley, Mary E.
 ; REGISTRATION NUMBER: 34,409
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (301) 258-5200
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:

Fri Feb 14 09:44:26 2003

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/ LENGTH: 1400 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA to mRNA
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ FRAGMENT TYPE: C-terminal
/ ORIGINAL SOURCE:
/ ORGANISM: Eimeria maxima
/ STRAIN: Houghton
/ DEVELOPMENTAL STAGE: sporozoite
/ IMMEDIATE SOURCE:
/ LIBRARY: sporozoite cDNA cloned in Lambda ZAPII
/ CLONE: Em70-1
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 1..1368
/
US-08-338-057-1

Query Match          9.4%; Score 165; DB 1; Length 1400;
Best Local Similarity 54.5%; Pred. No. 1.6e-32;
Matches 330; Conservative 0; Mismatches 275; Indels 0; Gaps 0;

QY 313 GAGCATCCAAATGTTGTAGGATCAAGGACTTATGAAGATTCGGTGTGTTTCATATT 372
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Db 151 GATCATCTTAATATCATGAATATATATGAATCTTTGAGGATAAGGATACCTTTATCTT 210

QY 373 GTTATGGAGTTTGTGAAGTGGTGGCTTTTGTATCGGATTCGATTCTTAAAGGTCATTTT 432
   |||||
Db 211 GTTACAGAAGTATATACAGGAGGAATTTTGTGAATTTAATTAATCGAAAAGATTC 270

QY 433 AGTGAAGCTGAAGCTCAAGCTTTAAGACGATTCCTGGTGTGTTGAGCGTTGTGCAT 492
   |||||
Db 271 AGCGAGCGGATCGACCTCGTATAGTACGTACGTTCTATCGGGTATAAATATATGCAT 330

QY 493 TCTCTTGGTGTATGATAGATCTCAACCTGAGATTTCTTGTGATAGTCTCTAAA 552
   |||||
Db 331 CGTAATAAATAGTTCATAGAGATTTAAAGCCAGAGAATTTATTATTAGAGAAATAAAAA 390

QY 553 GATGATGCTAAGCTTAAGCTACCGATTTTGGTGTGTTGTCTCTCTATATAAGCCAGGACAA 612
   |||||
Db 391 AAAGATGCAATATACGAATTTATGATTTGGGTATCTACACATTTTGAGCCCAAAA 450

QY 613 TATTTATAGCTAGTGTGAAGTCCGTAATCTATGTTGACAGAGTGTCTAAGAAATGT 672
   |||||
Db 451 AAAATGAAGGATAAAATCGGACCGGTACTACATTCGCCCTGAGGTGCTGACGGAACA 510

QY 673 TATGGACCTGAATAGATGTGAGTGTGTTGTATCTCTACATTTTACTCAGCGGT 732
   |||||
Db 511 TACGATGAGAAATGCGACGTCTGGTCTACGGGTGTTATCTCTATATCTTCTCTGTT 570

QY 733 GTTCCTCCCTTCTGGGAGAGACTGAGTCTGGAATCTTTAGACAGATATTGCAAGGGAAG 792
   |||||
Db 571 TGTCTCTCAATTAACGAGCAATGAATTTGAATTTCTAAAGAAAGTCGAGAAAGGAAAA 630

QY 793 TTAGATTTCAATCTGCCGCTGCCCTACTATCTCAGAGAGTGTAAAGATTGATCTAT 852
   |||||
Db 631 TTCACTTCGATTTACACAGTGGCGTTAGGTTAGCAGCCAGCAAGATTTAATTAGG 690

QY 853 AAAATGCTGAAAGGAGCCCAAGAACCCATTTCTGCTCATGAAGCCTTGTCACCCA 912
   |||||
Db 691 AAGATGTTAGCATATGATCCCTCAATGCCGTATATACGAAAGAGATGATATGATCATCCA 750

QY 913 TGGAT 917
   |||||
Db 751 TGGAT 755

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Search completed: February 13, 2003, 21:06:29
Job time : 103 secs

Result No.	Query %			DB	ID	Description
	Score	Match	Length			
1	1484.8	85.0	1488	9	US-09-938-842A-704	Sequence 704, App
2	744.2	42.6	1473	9	US-09-938-842A-786	Sequence 786, App
3	712.6	40.8	1635	9	US-09-938-842A-2344	Sequence 2344, App
4	643.4	36.8	1833	9	US-09-938-842A-2334	Sequence 2334, App
5	531.8	30.4	2230	10	US-09-828-313-26	Sequence 26, App
6	507.8	29.1	1638	9	US-09-938-842A-1859	Sequence 1859, App
7	448.2	25.7	455	10	US-09-770-444-571	Sequence 571, App
8	444.6	25.4	1602	9	US-09-938-842A-2304	Sequence 2304, App
9	277.8	15.9	1387	10	US-09-828-313-13	Sequence 13, App
10	227.4	13.0	955	10	US-09-770-445-326	Sequence 326, App
11	221.6	12.7	2253	10	US-09-828-313-25	Sequence 25, App
12	200.6	11.5	1800	9	US-09-938-842A-1063	Sequence 1063, App
13	193	11.0	718	9	US-09-938-842A-3678	Sequence 3678, App
14	189.6	10.9	2374	10	US-09-854-731-3	Sequence 3, App
15	168	9.6	413	10	US-09-878-574-3809	Sequence 3809, App
16	159.8	9.1	1372	10	US-09-817-181-1	Sequence 1, App
17	155	8.9	267	10	US-09-923-876-331	Sequence 331, App
18	145.6	8.3	1074	9	US-10-024-0368-3	Sequence 3, App
19	145.6	8.3	1578	10	US-10-024-0368-6	Sequence 6, App

QY 247 AAGCTCGTGTGCGGAGGATTAACGAATGATGCGGTGAGATTCAGATCATGATCAT 306
 Db 181 AAGCTCGTGTGCGGAGGATTAACGAATGATGCGGTGAGATTCAGATCATGATCAT 240
 QY 307 CTCTCTGAGCATCCAAATGTTGTTAGGATCAAGGAGCTTATGAAGATTCGGTCTTTGTT 366
 Db 241 CTCTCTGAGCATCCAAATGTTGTTAGGATCAAGGAGCTTATGAAGATTCGGTCTTTGTT 300
 QY 367 CATATTGTTATGGAGTTTGTGAAGTGGTGAAGTGGTGAAGTGGTGAAGTGGTGAAGT 426
 Db 301 CATATTGTTATGGAGTTTGTGAAGTGGTGAAGTGGTGAAGTGGTGAAGTGGTGAAGT 360
 QY 427 CATTTTAGTGAAGTGGTGAAGTGGTGAAGTGGTGAAGTGGTGAAGTGGTGAAGTGGT 486
 Db 361 CATTTTAGTGAAGTGGTGAAGTGGTGAAGTGGTGAAGTGGTGAAGTGGTGAAGTGGT 420
 QY 487 TGTCATCT 546
 Db 421 TGTCATCT 480
 QY 547 CCTAAGATGATGCTAAGCTTAAGCTTAAGCTTAAGCTTAAGCTTAAGCTTAAGCTTAAG 606
 Db 481 CCTAAGATGATGCTAAGCTTAAGCTTAAGCTTAAGCTTAAGCTTAAGCTTAAGCTTAAG 540
 QY 607 GGCAATATTATATGACGTAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 666
 Db 541 GGCAATATTATATGACGTAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 600
 QY 667 AATGTTATGACCTGAATAGATGCTGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 726
 Db 601 AATGTTATGACCTGAATAGATGCTGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 660
 QY 727 AGCGTGTCT 786
 Db 661 AGCGTGTCT 720
 QY 787 GGAAGTTAGATTCAAACTGACCGTGGCTTATCTATCTGAGAGCTGCTTAAGATTG 846
 Db 721 GGAAGTTAGATTCAAACTGACCGTGGCTTATCTATCTGAGAGCTGCTTAAGATTG 780
 QY 847 ATCTATAAATGCTCGAAGAGGAGCCCAAGAAAGCATTCTGCTCATGAAGCCTTGTGT 906
 Db 781 ATCTATAAATGCTCGAAGAGGAGCCCAAGAAAGCATTCTGCTCATGAAGCCTTGTGT 840
 QY 907 CACCCATGGAATGCTGATGAACAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 966
 Db 841 CACCCATGGAATGCTGATGAACAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 900
 QY 967 TCTCGTCTAAGCAGTCTCTCAATGAATGAATGAATGAATGAATGAATGAATGAATGAAT 1026
 Db 901 TCTCGTCTAAGCAGTCTCTCAATGAATGAATGAATGAATGAATGAATGAATGAATGAAT 960
 QY 1027 GCTGAGAGCTTTTTCAGAGGAGGAAATGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 1086
 Db 961 GCTGAGAGCTTTTTCAGAGGAGGAAATGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 1020
 QY 1087 ACAGACACAGCGGAAAGATTACTTTTGAAGCTCAAGCGGTTTGAAGAGTCGGA 1146
 Db 1021 ACAGACACAGCGGAAAGATTACTTTTGAAGCTCAAGCGGTTTGAAGAGTCGGA 1080
 QY 1147 TCTGAACCTGATGGAATCAGAAATCAAGTCTCTCATGATGCGGCTGATATCGACACAGT 1206
 Db 1081 TCTGAACCTGATGGAATCAGAAATCAAGTCTCTCATGATGCGGCTGATATCGACACAGT 1140
 QY 1207 GGTCAATATAGACTACGGAGATTCCTAGCAGCAACCTTACATGACAAAGATGGAGAGA 1266
 Db 1141 GGTCAATATAGACTACGGAGATTCCTAGCAGCAACCTTACATGACAAAGATGGAGAGA 1200
 QY 1267 GAGGAGATTCCTGGTGGCTGCAATTTTCGCACTTTTGAAGAGCAGGAGCGGTATATCACC 1326
 Db 1201 GAGGAGATTCCTGGTGGCTGCAATTTTCGCACTTTTGAAGAGCAGGAGCGGTATATCACC 1260

QY 1327 ATCGATGAGCTTCAGTTCAGCTTCAGAGAGTTTGTCTATGTATGATACACTCTGGACGAC 1386
 Db 1261 ATCGATGAGCTTCAGTTCAGCTTCAGAGAGTTTGTCTATGTATGATACACTCTGGACGAC 1320
 QY 1387 ATGATCAAGGAGATTCAGTTCAGCAATGACGGAAGATGATTTCTCGGAGTTTACAGCA 1446
 Db 1321 ATGATCAAGGAGATTCAGTTCAGCAATGACGGAAGATGATTTCTCGGAGTTTACAGCA 1380
 QY 1447 ATGATGAGGAAGAGATTCAGTTCAGCAATGACGGAAGATGATTTCTCGGAGTTTACAGCA 1506
 Db 1381 ATGATGAGGAAGAGATTCAGTTCAGCAATGACGGAAGATGATTTCTCGGAGTTTACAGCA 1440
 QY 1507 AACATTGCTGATGCTTTTGGAGTTGATGGTGAAGAAATCTGATGACTGA 1554
 Db 1441 AACATTGCTGATGCTTTTGGAGTTGATGGTGAAGAAATCTGATGACTGA 1488

RESULT 2
 US-09-938-842A-786
 ; Sequence 786, Application US/09938842A
 ; Patent No. US20020160378A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Harper, Jeff
 ; APPLICANT: Krops, Joel
 ; APPLICANT: Wang, Xun
 ; APPLICANT: Zhu, Tong
 ; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
 ; FILE REFERENCE: SRIPI300-3
 ; CURRENT APPLICATION NUMBER: US/09/938,842A
 ; PRIOR FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: US 60/227,866
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: US 60/264,647
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/300,111
 ; PRIOR FILING DATE: 2001-06-22
 ; NUMBER OF SEQ ID NOS: 5379
 ; SEQ ID NO 786
 ; LENGTH: 1473
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 US-09-938-842A-786

Query Match 42.6%; Score 744.2; DB 9; Length 1473;
 Best Local Similarity 70.0%; Pred. No. 3.4e-158;
 Matches 1001; Conservative 0; Mismatches 428; Indels 0; Gaps 0;

QY 106 GTTCTACCATATCAACACACCCAGATTAAGAGATCAATTACCTTCTGGGAAAAAGCTAGGC 165
 Db 28 GTTCTTCTCTTACAGACCAAAAACCGTTGAAGACAAATTACTTTTCTGGTCAAGTCTTTGGA 87
 QY 166 CAAGGCCAATTTGGACCAACCTTATCTCTGCACAGAGAATCAACCTCGCTAAATTACGCC 225
 Db 88 CAAGGCCAATTTGGACCAACCTTATCTCTGTACCCATAAACAGACAGGTCAAAGCTTGCC 147
 QY 226 TGCAAAATCGATCCGAGGCGAAAGCTCGTGTCTCGAGGATTACGAAGATGTATGGCGT 285
 Db 148 TGCAAAATCGATCCGAGGCGAAAGCTCGTGTCTCGAGGATTACGAAGATGTATGGCGT 207
 QY 286 GAGATTGAGATCATGATCATCTCTCTGAGCATCCAATGTTGTAGGATCAAGAGGACT 345
 Db 208 GAGATTCAGATAATGATCATCTCTGATTAATCCCAAGCTTCCCGTATAGAGAGTGG 267
 QY 346 TATGAAGATTCCGGTGTGTTGTTTCATATTGTTATGGAGGTTTGTGAAGGTTGGTGAAGCTTTT 405
 Db 268 TACGAGACACCAAAAACCGTGCATCTTGTGATGGAGCTTTGTGAAGGAGGTGAGTTGTT 327
 QY 406 GATCGGATTTCTTAAAGGTCAATTTTACTGAGCGTGAAGCTGTCAAGCTTATTAAAGCG 465
 Db 328 GATAGAATTCTGAAGAGAGGTCAATTACGTGAAGAGAGAGCTGCTTAAGCTTATCAAGACC 387
 QY 466 ATTCTTGGTGTGTTGAGGCTTGTCTTCTTCTTGTGTTTATGATGATGATGATCTCAAACT 525

Db 398 ATTGTTGGGTTGTTGAGCGTCTCACTCTCTGTTGTTTCATAGATCTTTAGCCT 447
 Qy 526 GAGAAATTTCTGTTTGTAGTCCCTAAAGATGATGCTTAAGCTTAAGGCTACCGATTTTGGT 585
 Db 448 GAGAAATTTCTGTTTGTCTCTGATGAAGATGCTCTCTTAATCTACTGACTTTGGC 507
 Qy 586 TTGCTGCTCTTCTATAAGCCAGGACAAATTTATATACGCTAGTTGGAAGTCCGTACTAT 645
 Db 508 CTCCTGTTTCTGCACACAGGAGAGCAATTTTCGGAATCTGTTGTAAGTCTTACTAT 567
 Qy 646 GTTGACACAGAGGTGCTAAAGAAATTTATGGAACCTGAAATAGATGTTGGAGTCTGGT 705
 Db 568 GTGGACCTGAGTTTACATAAGCAATTTATGCTCCTGAATGTCAGCTATGGAGTGTGGA 627
 Qy 706 GTTATCTCTACATTTTACTCAGGCGTCTCTCCCTCTGCGGACAGAGCTGAGTCTGGA 765
 Db 628 GTTATCTCTACATTTCTTATGTTGTTTCTCTCTTTTGGGCTGAGAGTGAATAGGC 687
 Qy 766 ATCTTTAGACAGATATTCGAAGGAAGTTAGATTTCAAACTGTACCCGTCGCTTACTATC 825
 Db 688 ATCTTCAGGAAGATTTACAGGAAGTTGAGTTTGAGATCAATCTTGGCCTAGCAAT 747
 Qy 826 TCAGAGCTGCTAAGATTTGATCTATAAATGCTCGAAGGAGCCCAAGAACCAAT 885
 Db 748 TCAGAGGTGCAAGATCTTATAAAGAAATGCTTGAAGCAATCTTAAAGAGGCTA 807
 Qy 886 TCTGCTCATGAAGCCTTGTGTCACCCATGATGCTGATGAACAGAGCAGCAGACAAAG 945
 Db 808 ACTGCTCATCAAGTGTGTCATCCGTTGATTTGGATGATAGGTTGCTCCAGATAA 867
 Qy 946 CTTCTGTATCCAGAGTCTTATCTGCTTAAGCAGATTTTCTCAATGAATAGATTAAG 1005
 Db 868 CTTTGGACTCGCGGTAGTGTCCGCTGAGAGTCTCTGCAATGAACAACTTAAG 927
 Qy 1006 AAAATGGCAATACGGTAAATCTGAGAGATTTTCAGAGGAAGAAATGGAGTCTGAAG 1065
 Db 928 AGATGGCTTTACGAGTATTTCAGAGAGACTATCTGAGGAAGAAATCGGTGCTCAAA 987
 Qy 1066 GAATTTGCTCAAGATGATAGACACAGAACAGCGAAGTATCTTTGAGAGCTCAAA 1125
 Db 988 GAACTGTTCAAAATGATAGACACAGATAAAAGTGGGACTATCAGCTTTGAGAGTTAAA 1047
 Qy 1126 GCGGTTTGAAGAGAGTCCGATCTGAATGGAATCAGAAATCAAGTCTCTCATGGAT 1185
 Db 1048 GATAGTATGAGAGTGTGGGTGAGAGCTTATGGAATCAGAGATCCAGAACTCTTGGCT 1107
 Qy 1186 GCGGTGATATCGAACACAGTGGTCAATAGACTACGAGAAATTCCTAGCAGCAACCTTA 1245
 Db 1108 GCGGCTGATGTTGATGAGAGTGAACAAATTCGATGAGAGTCTTAGCTGCAACAAATC 1167
 Qy 1246 CACATGAACAGATGAGAGAGAGAGATTTCTGGTGTGCTGATTTTCGACTTTGACAAA 1305
 Db 1168 CACTTGAACAGCTGGAGAGAGAGAGAAATCTAGTAGCTGCAATTTCTTTTGTATAG 1227
 Qy 1306 GACGAAGCGGTTATATCACCATCGATGAGTTCAGTCCAGCTTGCACAGAGTTTGGTCTA 1365
 Db 1228 GATGCAAGTGGTTACATCACTATCGAAGAGCTTCAACAGGCAATGGAAGGATTTGGTATA 1287
 Qy 1366 TGTGATACACCTCTGGAACAGATGATCAAGAGAGATTTGATGATGATGAGCGGAAGATC 1425
 Db 1288 AACGATTTCAATCTTGATGAATGATCAAGAGATTTGATCAAGATATGATGGAACAAAT 1347
 Qy 1426 GATTTCTCGAGTTTACAGCAATGATGAGGAAGAGAGATGGAGTTGGAGAGAGCAAGC 1485
 Db 1348 GACTATGAGAGAAATTTGTGCAATGATGAGGAAGAAATGCACTGGAGGAGGATTTGGT 1407
 Qy 1486 ATGATGAAGAACTTGAACTTCAACTTGTGATGCTTTTGGAGTTGATG 1534
 Db 1408 CGGAGAACTATAGGAACCTCTCTCAACTTTGGAACCTACTCTTCTCTGATG 1456

RESULT 3

US-09-938-842A-2344
 ; Sequence 2344, Application US/09938842A
 ; Patent No. US20020160378A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Harper, Jeff
 ; APPLICANT: Kreps, Joel
 ; APPLICANT: Wang, Xun
 ; APPLICANT: Zhu, Tong
 ; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
 ; TITLE OF INVENTION: SAME, AND METHODS OF USE
 ; FILE REFERENCE: SCRIPI300-3
 ; CURRENT APPLICATION NUMBER: US/09/938,842A
 ; CURRENT FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: US 60/227,966
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: US 60/264,647
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/300,111
 ; PRIOR FILING DATE: 2001-06-22
 ; NUMBER OF SEQ ID NOS: 5379
 ; SEQ ID NO 2344
 ; LENGTH: 1635
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 US-09-938-842A-2344

Query Match 40.8%; Score 712.6; DB 9; Length 1635;
 Best Local Similarity 68.3%; Pred. No. 4.6e-151;
 Matches 988; Conservative 0; Mismatches 459; Indels 0; Gaps 0;

Qy 73 ACGAAGCAACACCCCTAGACGCTCTTCAACACACAGATTTCTACCATATCAACACACCCAGATTA 132
 Db 184 ATGGGGGTAAAGTTGATGCAATCAATCTTACTATGTTCTGGTCACAGACTCCTAACAT 243
 Qy 133 AGAGATCATTAACCTTCTGGGAAAAAGCTAGGCCAAGGCCAATTTGGAAACAACTTATCTC 192
 Db 244 CGTGATCTTTACAGCTTGAGTCGTAGTTAGGACAAAGCAATTCGGGACCAAGCTATTG 303
 Qy 193 TGCACAGAGAAATCAACCTCGCTAATTTAGCCTCGAAATCGATCCGGAAGCGAAAGCTC 252
 Db 304 TGTACTGATATGCGCAGAGTGTGACTATGTTGATGTTAGTCTATATCCAGAGGAATTTG 363
 Qy 253 GTGTGTCCGAGGATTAACGAAGATGATGCGGTGAGATTCAGATTCAGATCATCTCTCT 312
 Db 364 ATATCTAAAGAAAGATGTTAGGATGTTAGGAGGAGATTCAGATTTATGATCATTTAGCT 423
 Qy 313 GAGCATCCAATGTTGTTAGGATCAAGGAGCTTATGAAGATTCGGTGTGTTGTTTCAAT 372
 Db 424 GGTCAAGAAATATTTGTTACTATTAAGGAGCTTATGAGGATCCTTTGTTATGTTACAT 483
 Qy 373 GTTATGAGAGTTCGTGAAGGTGGTGGCTTTTTCGCGGATTTCTTAAAGGTCAATTT 432
 Db 484 GTGATGAGCTTTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 543
 Qy 433 AGTGAGCTGAAGCTGCAAGCTTATTAAGACGATCTTGGTGTGTTGTTGAGGCTTGTCT 492
 Db 544 AGCGAGAGAAAGCTGCTGAGTTGACCAAGATCATTTGTCGGTGTGTTGAGGCGGTGCT 603
 Qy 493 TCTCTGTGTTTATGATAGATGATCTCAACCTCGAGAAATTTCTTGTGTTGATAGTCTCTAA 552
 Db 604 TCTCTGTGTTTATGATAGATTTAAAGCTGAGAAATTTCTTGTGTTTAAAGAT 663
 Qy 553 GATGATGTAAGCTTAAGGCTACCGATTTTGGTGTGTTGTTGTTGTTGTTGTTGTTGTTG 612
 Db 664 GATGATTTCTCTTTAAGGCCATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 723
 Qy 613 TATTTATATGAGTGTGGAAGTCCGCTACTATGTTGTCACAGAGGTGCTTAAAGAAATGT 672
 Db 724 ATATTAAGAGATGTTTGGAGTCCATCTATGTTGCTCTGAGGTTCTTCTTAAACAT 783
 Qy 673 TATGACCTGAAATAGATGTTGGAGTCTGTTGTTTATCTCTACATTTTACTCAGCGGT 732
 Db 784 TATGTCAGAGAGCTGATGTTGGAGTCTGTTGTTTATCTCTATATCTTACTTAAAGTGT 843

QY	733	GTTCCTCCCTTCTGGGCAGAGACTGAGTCTGGAACTTTTAGACAGATATTGCAAGGAG	792
Db	844	GTCCCGCCTTTCTGGGCAGAAACACAGCAGGAATAATTTGATGCTGTGTGAAGGGATAT	903
QY	793	TTAGATTTCAAAATCTGACCGCTGGCTACTATCTCAGAGCTGCTAAAGATTGTGATCTAT	852
Db	904	ATTGACTTTGATCAGACCCGCTGGCTGTCTATTCGACAGTCTAAAGATCTGATCCGG	963
QY	853	AAAATGCTCGAAAGGAGCCCAAGAAAACGATTTCTGCTCATGAAGCCTTGTGTCAACCA	912
Db	964	AAGATGTTATGCTCTAGTCTCTCTGAACGTTTGAAGTCTCATGAAGTCTTGCGTCAACA	1023
QY	913	TGGATTTGCTGATGAAACAGCAGACACAGAAAGCCCTTTGATCCAGCAGTCTTATCTCT	972
Db	1024	TGGATCTGTGAGAAATGAGATTGACCGGATAGAGCACTTGACCCGGCTGTTTGTCTCT	1083
QY	973	CTAAGCAGATTTTCTCAAAATGAATAAGATTAAAGAAAATGCAATTAACGGGTAAAT	1032
Db	1084	CTAAGCAGATTTTCTCAAAATGAATAAGATTAAAGAAAATGCAATTTAAAGGTGAT	1143
QY	1033	AGACTTTACAGAGGAAGAAATTTGAGGTTCTGAAGAAATTTTCAAGATGATAGACAGAC	1092
Db	1144	AGCCTCTCAGAAAGAGATTTGCGGTTTAAAGAGCAATTTTGAAGCAATTTGGAATCT	1203
QY	1093	AACAGCGGAACGATTAATTTTTGAAGACTCAAAAGCGGTTTGAAGAGAGTCGGATCT	1152
Db	1204	AACAGCGGTGCAATCACTTTTATGAACTCAAGCTGGCTTGAAGATATGGATCAACC	1263
QY	1153	CTGATGGAATCAGAAATCAAGTCTCTCATGATGCGGCTGATATCGACAAACAGTGT	1212
Db	1264	TTGAAGACACCGAGATCCGAGATCTTATGGAAGCGGCTGATGTGGAACAACAGCG	1323
QY	1213	ATAGACTACGGAGAAATTCCTAGCAGCAACCTTACACATGAACAGATGGAGAGAGAG	1272
Db	1324	ATAGATTACGCGAGTTTATTGACGACAGATCCATCTGAAATTAACCTAGAGAGAGAG	1383
QY	1273	ATTCTGTGGTGCATTTTTCGGACTTTTGACAAAGCAGGAAGCGGTTATATCACCAT	1332
Db	1384	CATCTTGTCTGCAATTTCACTTCTTTGACAAAGATGGAAGTGGTTACATCAGCA	1443
QY	1333	GAGCTTCAGTCAGCTTGACAGAGTTTGGTCTATGTGATACACCTCTGGACGACAT	1392
Db	1444	GAGCTGCACCAATCTTGCATTTGAACATGGGATGCCGATGTTTTTCTTGAAGACA	1503
QY	1393	AAGGAGATTGATCTTTGACAAATCAGCGGAAGATCGATTTCTCGGAGTTTACAG	1452
Db	1504	AAAGAGTAGATCAAGACACGATGGAACGATTTGATACGAAGAATTTTGTGCGAT	1563
QY	1453	AGGAAGAGATGAGATTGGGAGAGCAGAACCATGATGAAGAACTTGAACCTTCAAC	1512
Db	1564	CAAAAGGGAATGCTGGTGTAGGGAGAGAAACAATGAAAAATAGTCTAAACATCAG	1623
QY	1513	GCTGATG 1519	
Db	1624	AGAGATG 1630	
RESULT 4			
US-09-938-842A-2334			
; Sequence 2334, Application US/09938842A			
; Patent No. US20020160378A1			
; GENERAL INFORMATION:			
; APPLICANT: Harper, Jeff			
; APPLICANT: Kreps, Joel			
; APPLICANT: Wang, Xun			
; APPLICANT: Zhu, Tong			
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING			
; FILE OF INVENTION: SAME AND METHODS OF USE			
; FILE REFERENCE: SCRIPI300-3			
; CURRENT APPLICATION NUMBER: US/09/938.842A			
; CURRENT FILING DATE: 2001-08-24			
; PRIOR APPLICATION NUMBER: US 60/227,866			

Db 1682 CAACGAGTTTCATATCGGCAACAATGCACATGAACAGACGGAGAAAGAGATCACCTTTG 1741
Qy 1281 GCTGCTCAATTTTCGGAATTTGACAAAGAGCGGAGGGTTATATACCATCGATGAGTTTCA 1340
Db 1742 GGCAGCATTCATGCTATTCGACGGAACAATAGCGGGTATATCACCATCGACGAGTTCA 1801
Qy 1341 GTCAGCTTGACAGAGTTTGGTCTATGTGATAC---ACCTTGGACGACATGATCAAGGA 1397
Db 1802 GGAAGCAATGGAGAGAAATGGAATGGAGATCCTGAGACCATCCAAAGAGATCATCAGCGA 1861
Qy 1398 GATTGATCTTGACATGACGGGAGAGATCGATTTCTCGGAGTTTACAGCAATGATGAGAA 1457
Db 1862 GGTGACACAGACAACGACGGAGAGATGATGACAGAGTTCTGATGCCATGATGCCAA 1921
Qy 1458 AGGAGATGAGTTGGGAGAGACGAGAACCATGATGAAGAA 1496
Db 1922 GGGCAATCTCGCGCTGAAACCGGAGGAACGGTGAACAA 1960

RESULT 6
US-09-938-842A-1859
; Sequence 1859, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1859
; LENGTH: 1638
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1859

Query Match 29.1%; Score 507.8; DB 9; Length 1638;
Best Local Similarity 61.7%; Pred. No. 5,6e-105;
Matches 828; Conservative 0; Mismatches 507; Indels 6; Gaps 1;

Qy 131 TAAGAGATCATTAACCTTCTCGGMAAAGAGCTAGGCCAAGGCCAATTTGGAACAACCTATC 190
Db 176 TCAGCGCAAAATACATCTTAGTTCGTGAATTAGTTCGAGCGGAATTCGGAATCACTTACC 235
Qy 191 TCTGCACAGAGAATCAACCTCGCTAAATACGCTGCAAAATCGATCCGAGCGAAGC 250
Db 236 TCTGTACTGATCGTGAACCCAGAGCTTTAGCTTGCATAATCGATTCAAAGCGAAGC 295
Qy 251 TCGTGTCTCGGAGGATTACGAAGATGTATGCGGTGAGATTCAGATCATCATCTCTCT 310
Db 296 TTCGAACAGCTGTGATATCGAAGAGCTTCGTCGTAGGTAGCGATTATGTCTACTTTAC 355
Qy 311 CTGAGCATCAAAATGTTGTAGGATCAAGGGACTTATGAAGATTCGGTGTGTTTCATA 370
Db 356 CTGAGCATCAAAAGCTAGTTAAGCTTAGCTAGTTATGAGGATAAGAGACGTCGATC 415
Qy 371 TTGTTATGAGAGTTTGTGAAGGTGGTGAAGCTTTTTCATCGGATTTGTTCTAAAGTCAAT 430
Db 416 TGGTTATGAGACTTTGTGAAGGAGGTGAGCTTTTTCATCGGATTTGTTCTAGAGACAT 475
Qy 431 TTAGTGAGCGTGAAGCTGTCAAGCTTTATTAAGACGATTTCTGGTGTGTTGAGGCTTCTC 490

RESULT 7
US-09-770-444-571

Db 476 ACACGAGCGTGTCTGCTGAGCTGTTGCGAGAACGATTTGCTGAGGTTGTGATGATGTC 535
Qy 491 ATTCTCTTGGTGTATGATAGATGATCTCAACCTGAGAAATTTCTTGTGATGATGCTTA 550
Db 536 ACTCTAATGGAGTTATGATCGAGATTTGAAACCTGAGAAATTTCTTGTGTAATAAAA 595
Qy 551 AAGATGATGCTAAGCTTAAGGCTACCGATTTTGGTGTGCTGCTTCTATTAAGCCAGGAC 610
Db 596 AGGAGAAATCTCCACTAAAGGCTATTTGATTTTGGCTTGTGCTGTTCTTCAACCTGGAG 655
Qy 611 AATATTTATGACGTAGTTGGAAGTCCGTACTATGTTGCACAGAGGTGCTTAAAGAAAT 670
Db 656 ATAAATTTACAGAGATTTAGGAAGTCCGTATTTATATATATGCTCCAGAAAGTGTGAAGAG 715
Qy 671 GTTATGACCTGAAATAGATGTGGAGTCTGCTGTATCCCTCTACATTTTACTCAGCG 730
Db 716 ATTATGGACAGGGGTTGATGTGGAGTCCCGAGTTATATCTATATCTTCTGCTCTGTG 775
Qy 731 GTGTTCTCTCCCTTCTGGGACAGACTGAGTCTGGAATCTTTAGACAGATATTGCAAGGA 790
Db 776 GTGTTCTCTCCGTTTTTGGCTGAGACTGAACAAGTGTGCTCTTGGGATCTTGGCGGAG 835
Qy 791 AGTTAGATTTCAAATCTGACCCGTGGCTACTATCTCAGAGCTGCTAAAGATTTGATCT 850
Db 836 TTCTTGATTTTAAAGAGAGACCTTTGGCTTCAAGATATCAGAGATGCGAAGAGCTTGTGA 895
Qy 851 ATAAATGCTCGAAAGGAGCCCAAGAAACGCATTTTCTGCTCATGAAGCCTTTGTGTACC 910
Db 896 AGCAGATGTTGATCTGATCCGACTAAGCGGTTAACTGCTCAGCAAGTGTAGCTCACC 955
Qy 911 CATGATTTGCTGATGAACAGCAGCACCACAGAGCTCTTGATCCAGAGCTTTATCTC 970
Db 956 CATGATACAGATGCAAGAAAGCTCCCAATGTCCTTTAGGAGATATAGTCAGATCTA 1015
Qy 971 GTCTAAAGCAGTTTTCTCAAATGAATGAATTAAGAAATGGAATTTACGGGTAAATGCTG 1030
Db 1016 GGTTCAGAGCTTCTCTATGATGAACAGATTCAAAAGABAGTTCITCGTAAATGCGG 1075
Qy 1031 AGAGACTTTCAGAGGAAGAAATTCGAGCTCTGAAGGAATTTGTTCAAGATGATAGACAG 1090
Db 1076 AGCACTTGTCTATTCAAGAGGTGAAGTGATAAAGAACATGTTCTCTACTGATGATG 1135
Qy 1091 ACAACAGCGGAACGATTAATTTTGAAGAGCTCAAGCGGTTTGAAGAGAGTCGGATCTG 1150
Db 1136 ACAAGATGTTAAATTAATTTACCGGNACTCAAGAGTGGCTTCAAGAGTGGTTTAC 1195
Qy 1151 AACTGATGGAATCAGAAATCAAGTCTCTCATGATGCGGTGATATCGACAAAGTGGA 1210
Db 1196 AACTTGGTGAACAGAGATCAAAATGTTGATGGAAGTGGCGGATGTCGATGGAAATGGT 1255
Qy 1211 CAATAGACTACGGGAATTTCTCTAGCAGCAACCTTACACATGAACAAGATGGAGAGAG 1270
Db 1256 TTCTGATTTATGAGAGATTTGATGCTGTGATTAATCTACTTGCAGAGATAGAGATGATG 1315
Qy 1271 AGATTCTGTGCTGCTCAATTTTGGGACTTTTGAAGAAGCGGAGCGGTTATATCACCATCG 1330
Db 1316 AACTTTTCAAACTAGCTTTTATGTTTTTCGACAAAGATGGAAGTACATACATTTGAAC 1375
Qy 1331 ATGAGCTTCAGTCACTTTGCACAG-----GTTTGGTCTATGTGATACACCTCTGGACG 1384
Db 1376 ATGAGCTACGGGAAGCTTTAGCGGATGAGTTAGCGGAGCCAGACCCAGCTGTCTAAGCG 1435
Qy 1385 ACATGATCAAGGAGATTTGATCTTGACAAATGACGGGAAGATCGATTTCTCGAGGTTTACAG 1444
Db 1436 ACATCATGCGTGAAGTTGACACTGACAGGAGCGGAGCGTATAAACTATGATGAGTTTGTGA 1495
Qy 1445 CAATGATGAGGAAGGAGATG 1465
Db 1496 CGATGATGAAGCTGGAATG 1516

; Sequence 571, Application US/09770444
; Patent No. US2002023280A1
; GENERAL INFORMATION:
; APPLICANT: Gorlach, Jörn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Ramekha, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Krickler, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; TITLE OF INVENTION: thaliana
; FILE REFERENCE: 2027 (PARA-016PRV)
; CURRENT APPLICATION NUMBER: US/09770,444
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,502
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 571
; LENGTH: 455
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; NAME/KEY: misc_feature
; LOCATION: (1)...(455)
; OTHER INFORMATION: n = A,T,C or G
US-09-770-444-571

Query Match 25.7%; Score 448.2; DB 10; Length 455;
Best Local Similarity 98.9%; Pred. No. 8.6e-92;
Matches 450; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 999 GATTAAAGAAATGGCAATTCACGGTAATTGCTGAGAGACTTTTCAGAGAGAAATTCGAGG 1058
Db 1 GATTAAAGAAATGGCAATTCACGGTAATTGCTGAGAGACTTTTCAGAGAGAAATTCGAGG 60
Qy 1059 TCTGAAGGAATGTTCAAGATGATAGACACAGACACAGCGGACGATTACTTTTGAGA 1118
Db 61 TCTGAAGGAATGTTCAAGATGATAGACACAGACACAGCGGACGATTACTTTTGAGA 120
Qy 1119 GCTCAAGCGGTTTGAAGAGAGTCCGATCTGAACTGATGAATCAGAAATCAAGTCTCT 1178
Db 121 GCTCAAGCGGTTTGAAGAGAGTCCGATCTGAACTGATGAATCAGAAATCAAGTCTCT 180
Qy 1179 CATGATCGGCTGATATCGACACAGTGGTACATAGACTACGGAATTCCTAGCAGC 1238
Db 181 CATGATCGGCTGATATCGACACAGTGGTACATAGACTACGGAATTCCTAGCAGC 240
Qy 1239 AACCTTACATGAACAGATGGAGAGAGAGAGATTCTGGTGGCTGCATTTTCGGACTT 1298
Db 241 AACCTTACATGAACAGATGGAGAGAGAGAGAACTCGTGGCTGCATTTTCGACTT 300
Qy 1299 TGACAAAGCGGAGCGGTTATATCACCATGATGAGTTCAGTTCAGTTCGACAGATT 1358
Db 301 TGACAAAGCGGAGCGGTTATATCACCATGATGAGTTCAGTTCAGTTCGACAGATT 360
Qy 1359 TGGTCTATGTGATACACCTTCGAGAGATGATCAAGAGATTGATCTTGACATGACGG 1418
Db 361 TGGTCTATGTGATACACCTTCGAGAGATGATCAANNAGATTGATCTTGACATGACGG 420

Qy 1419 GAAGATCGATTTCTCGAGGTTTACAGCAATGATGA 1453
Db 421 GAAGATCGATTTCTCGAGGTTTACAGCAATGATGA 455
RESULT 8
US-09-938-842A-2304
; Sequence 2304, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCDP1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2304
; LENGTH: 1602
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2304

Query Match 25.4%; Score 444.6; DB 9; Length 1602;
Best Local Similarity 59.7%; Pred. No. 9.4e-91;
Matches 788; Conservative 0; Mismatches 524; Indels 9; Gaps 2;
Qy 142 TACCTTCTGGGAAAAAGCTAGCCCAAGGCCAATTTTGGACACACCTATCTCTGCACAGAG 201
Db 169 TATGATCTGGGGCGTGAGGTGTGCGGAGAGTTTGGTATTACTTGTGCTGACTGAT 228
Qy 202 AAATCAACCTCCGCTAATTACGCTTGCATTCGAAATCGATCCGAAGCGAAAGCTCGTGTGCG 261
Db 229 ATCAAAACGGCGGAGAGTATGCGTCAAGTCTATATCAAGAAGAAGCTTAGAACAGCT 288
Qy 262 GAGGATTCAGAGATGATGGGTGAGATTGAGATCATGATCATCTCTCTGAGCATCCA 321
Db 289 GTGATATAGAGGATGTTAGGAGGAGTTGAGATAATGAACATATGCTTAGACACCCA 348
Qy 322 AATGTTGTAGGATCAAGGAGCTTATGAAGATTCCGTTGTTGTTTCATATTGTTATGGAG 381
Db 349 AATATCGTGTGCTGAAGGATGCTTTGAGATGATGATGCGATGATATAGTTATGGAG 408
Qy 382 GTTTGTGAAGGTGCTGAGCTTTTGTGATCGGATTTGTTCTTAAGGTCAATTTAGTGAGCGT 441
Db 409 TTGTGTGAAGGAGTGAGCTGTTTGTGATCGGATTTGTTGCTAGAGGTCAATTTAGTGAGCGA 468
Qy 442 GAAGCTGTCAAGCTTATTAAGAGCATTTCTTGGTGTGTTGTTGAGGCTTGTCTCTTGTGT 501
Db 469 GCTGCTGCTGAGTATGAAGACATATCTTTGAAGTGTTCAGATATGCCATGAAGCATGA 528
Qy 502 GTTATGATGATGATCTCAAAACCTCGAGAATTTCTGTTGATAGTCTCTAAAGATGATGCT 561
Db 529 GTGATGATCGGATCTAAAGCCTCGAGAACTTTCTCTTTCGAAATAAAAGAGACATCA 588
Qy 562 AAGCTTAAGCTACCGATTTTGGTGTGCTGCTCTTATTAAGCCAGAGCAATATTATAT 621
Db 589 GCCCTTAAGCCATAGATTTTGGATTCAGTCTTCTTAAGCTCTGTGAGGATTCAC 648
Qy 622 GACGTAGTTGGAAGTCCGCTACTATGTTGACACGAGGTGCTAAAGAAATGTTATGGACCT 681
Db 649 GAGATGTTGGAAGTCCCTTATACATGCGACAGAGGTACTTAGGCGAAATACGGACCT 708
Qy 682 GAATAGATGTTGAGAGTGGTGTGTTATCCTCTACTATTCTAGCGGTGTTCTCCTCC 741

Db 1044 ACCTACATTTTCTATGTGTAGTGCACCGTTTGGGCGCGGACCGAGTCGGGCAITTTT 1103
 QY 772 AGACAGATATTCAGAGGAGTAGATTCAAACTGACCCGCTGCTACTATCTCAGAA 831
 Db 1104 CTTGGCGGTGTTAGGGCTGACCCGAGCTTTGAGAGCCCTTTGGCTTCACTCTCCC 1163
 QY 832 GCTGTAAAGATTTGATCTATAAAATGCTGAAAGGAGCCCAAGAAACGATTTCTGCT 891
 Db 1164 GAAGCCAGGATTTCTGTGAAGGCTCTCTGAAATAGGATATGCGGAAACGATGCT 1223
 QY 892 CATGAAGCTTTGTCACCCATGATTTGCGATGACAGCAGCAGCAGCAGCCTCTT 951
 Db 1224 GCACAAGCTTTAATCATCATCCATGATTTGAGTAAACAG-----TGAAGTACCTCTG 1277
 QY 952 GATCCAGCAGTCTTATCTCTGCTTAAAGCAGTTTCTCAATGAATAAGATTAAGAAATG 1011
 Db 1278 GATATCTTAGTGTACAGACTTTGTGAGGAATATCTCTGTCATCATCCATGAGAAAGCT 1337
 QY 1012 GATTTAGGGTAAATGCTGTAGAGACTTTTTCAGAGGAGAAATTTGAGGCTCAGAGAAATG 1071
 Db 1338 GCTTTGAAGGCGCTGCTCAAGACTTTTAAACGAGAGCAGACTTTTATCTACGTAACAA 1397
 QY 1072 TTCAAGATGATAGACACAGACACAGCAGGAGAACTTTTGAAGAGCTCAAGAGCGGT 1131
 Db 1398 TTTATGCTCTAGAACCAAGTAACACGCTGCTGTACTTTTGAATTTTCAGACAGCA 1457
 QY 1132 TTGAAGAGAGTCGGATCTGAATGATGAA 1161
 Db 1458 CTGCTGAAAAAATTCACAGAGGCCATGAAA 1487

RESULT 12
 US-09-938-842A-1063
 ; Sequence 1063, Application US/09938842A
 ; Patent No. US20020160378A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Harper, Jeff
 ; APPLICANT: Kreps, Joel
 ; APPLICANT: Wang, Xun
 ; APPLICANT: Zhu, Tong
 ; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
 ; FILE REFERENCE: SAME, AND METHODS OF USE
 ; CURRENT APPLICATION NUMBER: US/09/938,842A
 ; PRIOR FILING DATE: 2001-08-24
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR FILING DATE: 2001-06-22
 ; NUMBER OF SEQ ID NOS: 5379
 ; SEQ ID NO 1063
 ; LENGTH: 1800
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 US-09-938-842A-1063

Query Match 11.5%; Score 200.6; DB 9; Length 1800;
 Best Local Similarity 52.4%; Pred. No. 8.1e-36;
 Matches 490; Conservative 0; Mismatches 439; Indels 6; Gaps 2;

QY 229 AATGATCCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 288
 Db 526 AAGATCATCCCAAAATCTAAGATGACATCTGCAATATCTATAGAGGATGAGAGAGAA 585
 QY 289 ATTGATCATGATCATCTCTGATGATCCAAATGTTTGTAGGATCAAGAGGAGGAGGAGGAG 348
 Db 586 GTGAAATCTGCGGCGTTATCTGGACATCAAAATTTGTACAAATCTATGATGCTTC 645
 QY 349 GAAGATTCGGTGTGTTTTCATATTTGATGAGGTTTGTGAAGTGTGAGCTTTTGTAT 408

Db 646 GAGGACAAATGCCAACGTTTACATCGTTATGAGGTTATGAGGAGTGGTGAACCTTCTTGAC 705
 QY 409 CGGATTTGTTCTA---AAGTCAATTTTAGTGAAGCTGCAAGCTTCAAGCTTATTAAAGAG 465
 Db 706 AGGATCTAGCAAGGGAGGAAATATCTCTGAAGATGATGCAAAAGCAGTGTCTTATACAG 765
 QY 466 ATTTCTGGTGTGTTGAGGCTTGTCTCTCTTTGTTGTTATGATGATAGAGATCTCAAACT 525
 Db 766 ATCTTTAAGCTGTAGCTTTCTGTCTCTCAAGGAGTGTCTCATCGAGATCTAAACCA 825
 QY 526 GAGAAATTTCTTTGTTGATGCTTAAAGATGATGCTAAAGCTTAAAGCTTAAAGCTTAAAGCT 585
 Db 826 GAGAACTTTCTTTGATCTTCAAGGAGGAGAAATCTATGTTGAAAGCTATAGATTTTGGC 885
 QY 586 TTGCTGTCTCTTATAGCCAGGAGCAATATTTATGACGTAGTTGGAAGTCCGTACTAT 645
 Db 886 TTATCGGACTTTGTGACAGCAGCAAGAACTAAATGATATAGTGGAGTGCATATTAC 945
 QY 646 GTTGACACAGAGGTGCTAAAGAAATGTTATGACCTGAAATAGATGTGAGAGTGTGTT 705
 Db 946 GTAGCCCTGAGTTCTACACAGATCTTATACCACAGAGCGGATGTATGAGCATAGGA 1005
 QY 706 GTTATCTCTACATTTTACTCAGCGGTGTTCTCTCCCTTCTGGCAGAGACTGAGTCTGGA 765
 Db 1006 GTCATAGCATACATTTCTCTATGTGGAAGCGCTCTTTTGGCAGAACTGAATCAGGA 1065
 QY 766 ATCTTTAGACAGATTTGCAAGGGAAGTTAGATTTCAAAATCTGACCCGTCGCTACTATC 825
 Db 1066 ATTTTCAGACAGTTCTTAAAGCTGATCCCGATTTTGTGAACTCTCTGCTTCTGTTA 1125
 QY 826 TCAGAGCTGTAAAGATTTGATCTATAAATGCTCAAGAGGAGCCCAAGAAACGCAAT 885
 Db 1126 TCCCTTTGAGGCAAAAGATTTGTTAAGAGATTTATGACAGGAGCCCTCGGAAAGAAATG 1185
 QY 885 TCTGCTCATGAAGCCTTGTGACCCATGAGATTTCTGATGAAACAGCAGCAGCAGCAAG 945
 Db 1186 ACTGATCTCAGCTTTGATGATCTCTGATCGGGTTATA--GAAATAGATATC 1242
 QY 946 CTTCTGATCCAGAGCTTTATCTGCTTAAAGCAGTCTTCTCAAAATGAATAGATTAAG 1005
 Db 1243 CCATTTGATATTTCTGATCTTCAAGCAGATCAAGCATACTTTGAGATCTTCTGCTTCGCG 1302
 QY 1006 AATATGGCATTCAGGTAATTTCTGAGAGACTTTTCAAGAGGAGAAATTTGAGGTTCTGAAG 1065
 Db 1303 AAGCTGCTTTGATGCTCTGCTGCTCAAGACATTAATACCAGTGAACITCTTATCTGAA 1362
 QY 1066 GAATTTTCAAGATGATAGACACAGCAACAGCGGAGAGATTTCTTTGAAGAGCTCAA 1125
 Db 1363 GCGCAGTTTGCACACTTAGCACCCCAAAATGCGCTCATCACTTTTAGATAGCATCAGA 1422
 QY 1126 GCGGTTTGAAGAGAGTGGATCTGAACTGATGGA 1160
 Db 1423 CTGGCATTGCGCAAAATGCAACAGAGCAATGAA 1457

RESULT 13
 US-09-938-842A-3678
 ; Sequence 3678, Application US/09938842A
 ; Patent No. US20020160378A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Harper, Jeff
 ; APPLICANT: Kreps, Joel
 ; APPLICANT: Wang, Xun
 ; APPLICANT: Zhu, Tong
 ; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
 ; FILE REFERENCE: SAME, AND METHODS OF USE
 ; CURRENT APPLICATION NUMBER: US/09/938,842A
 ; PRIOR FILING DATE: 2001-08-24
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 3678
; LENGTH: 718
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-3678

Query Match 11.0%; Score 193; DB 9; Length 718;
Best Local Similarity 100.0%; Pred. No. 2.8e-34;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1555 CTCATCATCTTCCACAAATTCCTGTTTTTCTCTTAATTCGTTTATATTTGAAT 1614
DB 1 CTCATCATCTTCCAAATTTCTGTTTTTCTCTTAATTCGTTTATATTTGAAT 60
QY 1615 CTAATTTCTAAGGATACAAAATATATTCCTGCTGTTTTTCTCTTTTATTTT 1674
DB 61 CTAATTTCTAAGGATACAAAATATATTCCTGCTGTTTTTCTCTTTTATTTT 120
QY 1675 GTACATGAGCACTTCTAAATTTTATCTCTCATATGATAAATTTTGTCTCATATAAAA 1734
DB 121 GTACATGAGCACTTCTAAATTTTATCTCTCATATGATAAATTTTGTCTCATATAAAA 180
QY 1735 GTTTTGAATCC 1747
DB 181 GTTTTGAATCC 193

RESULT 14
US-09-854-731-3
; Sequence 3, Application US/09854731
; Patent No. US20020120949A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Lee, Jian Ming
; TITLE OF INVENTION: Plant Protein Kinases
; FILE REFERENCE: BB-1171
; CURRENT APPLICATION NUMBER: US/09/854,731
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/092,438
; PRIOR FILING DATE: July 10, 1998
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 3
; LENGTH: 2374
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-854-731-3

Query Match 10.9%; Score 189.6; DB 10; Length 2374;
Best Local Similarity 53.8%; Pred. No. 2.7e-33;
Matches 440; Conservative 0; Mismatches 369; Indels 9; Gaps 2;

QY 271 GAAGATGATGCGGTGAGATTCAGATCATGATCATCTCTGAGCATCCAAATGTGTT 330
DB 846 GAGGATGTTCTGAGAGAAGTAAATTTTGAGCGGTATCAGGSCACATAATCTCGTC 905
QY 331 AGGATCAAAGGACATTATCAAGATTTCGGTGTGTTGTTTCATATTGTTATGAGGTTTGTGAA 390
DB 906 AAATTTCTATGATGATGTGAGGATGCGCTCAATGCTACATTTGTCATGGAATTTATGTGAG 965
QY 391 GTGTGTGAGCTTTTGTAGCGGATGTTTCTAAAGTCAATTTAGTAGCGGTGAGCTGTC 450
DB 966 GGAGGAGAATTGCTAGACAGAAATATTAGCCAGAGCGGGAGATACACAGAGGAAGATGCC 1025
QY 451 AA---GCTATTAAACAGATCTTGGTGTGTTGTTGAGGCTTGTCTATTCTCTTGTGTTATG 507
DB 1026 AAAGCGATTGTTGACAGATTGAGCGGTAGTAGCCITCTGTCACTTCAGGGGTAGTG 1085
QY 508 CATAGAGATCTCAAACCTGAGAAATTTCTTGTGTTGATAGTCTCAAGATGATGCTAAGCTTT 567

DB 1086 CATCGTGATTGAAGCCAGAGAAATTCCTTTTCAACACCGAGGATGAATAATGCTCCCATG 1145
QY 568 AAGCTACCGAATTTGGTTGCTGCTCTATATAAGCCAGGACAATATTATATATGACGTA 627
DB 1146 AAGTTGATTGATTTGGTCTCTCTGATTTCAITAGACAGATGAAAGGCTTAATGATATT 1205
QY 628 GTTGGAAAGTCCGTACTATGTTGACACAGAGGTGCTAAAGAAATGTTATGACCTGAAATA 687
DB 1206 GTTGGAAAGTGCATATATTATGTTGCCACAGAGGTTTACACAGATCATATAGTATGGAAGA 1265
QY 688 GATGTGGAGTGTGCTGTTATCTCTCTACATTTTACTCAGCGGTGTTCTCTCCCTCTGG 747
DB 1266 GACATTTGGAGTATAGTGTGCTAAAGTACATTTCTGCTCTGTGGCAGTCGGCCATTCTGG 1325
QY 748 GCAGAGACTGAGTCTGGAATCTTTAGACAGATATTTCAGAGGAAGTTAGATTTCAATCT 807
DB 1326 GCAGAAACAGAAACAGGAATATTCGATCTGTGTGAGAGCTGATCCCACTTTTGATGAT 1385
QY 808 GACCCGTGGCTTACTTCTCAGAAAGCTGCTAAAGATTTGATCTATAAAATGCTCGAAAGG 867
DB 1386 TCACCGTGGCTACAGTATCAGCTGAAGCTAAGGATTTTGTGAAGAGATTTCTGAACAAA 1445
QY 868 AGCCCAAGAAAGCAATTTCTGCTCATGAAGCCTTGTGTCAACCATGGAATTTGCGATGA 927
DB 1446 GATTACCGCAAAAGAAATGACCGCTGTTCAAGCACTGACTCATCTTTGGTTGCGAGATGA 1505
QY 928 CAAGCAGACCCAGACAAAGCCTTTGATCCAGCAGTCTTATCTCGTCTAAAGCAGATTTTCT 987
DB 1506 CA-----RAGCGAGATCCCGCTGGACATACATCTTCAGATTAATTAAGCAATACCTC 1559
QY 988 CAAATGAATGAATTAAGAAATAGGCAATTAACGGTAAATTCGCTGAGAGACTTTTCAGAGGAA 1047
DB 1560 CGCCTACAGCTCTTAAACGGTTGGCAATTAAGGCACTATCAAGGCTTTAAGGGAAGAT 1619
QY 1048 GAAATTCGAGTCTGAGGAATTTTCAAGATCATAGA 1085
DB 1620 GACTTTTGTATCTCAAACTGCGAGTTTAACTGCTCGA 1657

RESULT 15
US-09-878-574-3809
; Sequence 3809, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 3809
; LENGTH: 413
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-005-Q1-B1-B8
US-09-878-574-3809

Query Match 9.6%; Score 168; DB 10; Length 413;
Best Local Similarity 63.2%; Pred. No. 9.5e-29;
Matches 258; Conservative 0; Mismatches 150; Indels 0; Gaps 0;
QY 834 TGCTAAAGATTGATCTATAAATGCTCGAAAGAGCCCCCAAGAAACGCAATTTCTGCTCA 893
DB 4 TGCTAAAGACCTAGTCAGGAAGATGCTGACACAGGATCCAAACAGCGGATTAATCTTCTC 63
QY 894 TGAAGCCTTGTGTACCCATGGATTGTCGATGAACAGCAGCAGACAGCAAGCCCTTGA 953
DB 64 TCAAGTCTCTGAACACCCATGGATGAGAGAAGGTGAGATGATCTGATAAACCAATCGA 123

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QY 954 TCCAGAGCTTATCTCTCTAAGCAGTTTTCTCAAAATGAATTAAGAAATGGC 1013
Db 124 TAGTGCAGTTCTATCCAGAATGAACAATTCAGGGCAATGATTAAGCTCAAGAGCTAGC 183
QY 1014 ATTACGGGTAAATTGTGTAGAGACTTTTCAGAGAAAGAAATTCGAGGCTCTGAAGGAATGTT 1073
Db 184 AATTGAAGGTTATCGCTGAAAATCTATCAGAAGAGGAGATTAAAGGTCTCAAAGCAATGTT 243
QY 1074 CAAGATGATAGACACAGACAAACAGCGGAAACGATTACTTTTGAAGAGCTCAAAGCGGTTT 1133
Db 244 TGCCAACTGGACACTGACATATAGTGGCACTATCACCTATGAAAGATTAAGACTGSCIT 303
QY 1134 GAAGAGAGTCGGATCTGAACTGATGGAATCAGAAATCAAGTCTCTCATGATGGGCTGA 1193
Db 304 GGCTCGAATCGGATCAAAACTGCTGAGGCTGAAGTGAAGCAACTCATGGATGGGCTGA 363
QY 1194 TATCGAACACAGTGGTACATAGACTACGGAGAAATTCCTAGCAGCAAC 1241
Db 364 TGTGACGGAAATGGGTGATTGACTATCTTGAATTCATTTCCGGGTAC 411

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GenCore version 5.1.3
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: em_estinv:*

4: em_estmus:*

5: em_estpl:*

6: em_estpro:*

7: em_estrod:*

8: em_estst:*

9: gb_est1:*

10: gb_est2:*

11: gb_est3:*

12: gb_est4:*

13: gb_est5:*

14: gb_est6:*

15: em_estfun:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pln:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_mam:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	563.4	32.2	591	10	AV825282 AV825282
3	523.6	30.0	2566	11	AY109374 Zea mays
4	505.8	29.0	2298	11	AY109401 Zea mays
5	503.8	28.8	507	10	AV558412 AV558412
6	484	27.7	835	12	BG647837 EST509456

c	7	480.6	27.5	1628	11	AY109463
c	8	466.8	26.7	814	12	BG887873
c	9	439	25.1	493	17	B28263
c	10	437.8	25.1	1087	17	B11596
c	11	424.8	24.3	528	9	A1994248
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c	15	388.8	22.3	751	14	BQ863474
c	16	379.2	21.7	723	14	BQ986998
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c	18	374.2	21.4	695	14	BQ115699
c	19	374	21.4	421	10	AV790851
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c	40	330.4	18.9	554	9	A1894480
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c	43	322.8	18.5	698	12	BQ592994
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ALIGNMENTS

RESULT 1
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LOCUS AY109473 2380 bp mRNA linear HTC 25-MAY-2002
DEFINITION Zea mays CL1905_1 mRNA sequence.
ACCESSION AY109473
VERSION AY109473.1 GI:21213206
KEYWORDS HTC.
SOURCE Zea mays.
ORGANISM Zea mays

REFERENCE
AUTHORS
Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,
Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 2380)

Maize Mapping Project/DuPont Consensus Sequences for Design of
Overgo Probes

Unpublished (2002)

2 (bases 1 to 2380)

Coe,E.C.

Direct Submission

Submitted (25-APR-2002) Maize Mapping Project, University of

Missouri, Columbia, MO 65211, USA

Location/Qualifiers

1. .2380

/organism="Zea mays"

/db_xref="MaizeDB:630671"

/db_xref="taxon:4577"

/clones="CL1905_1"

FEATURES		Location/Qualifiers		TITLE		Maize Mapping Project/DuPont Consensus Sequences for Design of	
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		/db_xref="taxon:3702"		2 (bases 1 to 2566)			
		/clone="RAFLO7-07-K16"		AUTHORS		Coe,E.C.	
		/clone_lib="RAF17"		TITLE		Direct Submission	
		/dev_stage="rosette plants"		JOURNAL		Submitted (25-APR-2002) Maize Mapping Project, University of	
		/lab_host="DH10B"		FEATURES		Missouri, Columbia, MO 65211, USA	
		/note="Site 1: BamHI; Site 2: SalI; subjected to cold-treated (1, 2, 5, 10, 24 hr)"		Location/Qualifiers			
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ORIGIN							
Query Match	32.2%; Score 563.4; DB 10; Length 591;						
Best Local Similarity	98.8%; Pred. No. 4.7e-93;						
Matches 567; Conservative	0; Mismatches 7; Indels 0; Gaps 0;						
QY	8 GTACATATTCCTTCTTCTTCTTCAAAATCGAGATCGAAGAGAACCAACAAAAACCAAAAA 67						
Db	18 GTTATCATCTCTTCTTCTTCTTCAAAATCGAGATCGAAGAGAACCAACAAAAACCAAAAA 77						
QY	68 TGGAGACGAAGCAAAACCTAGACGCTCTTCAACACACAGTTCTTACCATATCAACACACAC 127						
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QY	128 GATTAGAGATCATTTACCTTCTGGGAAAAAAGCTAGGCCAAGGCCAAATTTGGAACAACCT 187						
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QY	188 ATCTCTGCACAGAGAAATCAACTCCGCTAATTACGCTCGCAATTCGATCCCGAAGCGAA 247						
Db	198 ATCTCTGCACAGAGAAATCAACTCCGCTAATTACGCTCGCAATTCGATCCCGAAGCGAA 257						
QY	248 AGCTCGTGTGCGGAGGATTACGAGATGATGCGTGGAGATTCAGATCATGATCATC 307						
Db	258 AGCTCGTGTGCGGAGGATTACGAGATGATGCGTGGAGATTCAGATCATGATCATC 317						
QY	308 TCTCTGAGCATCCAAATGTTGTAGGATCAAAAGGACTTATGAGATTCGGTGTGTTGTC 367						
Db	318 TCTCTGAGCATCCAAATGTTGTAGGATCAAAAGGACTTATGAGATTCGGTGTGTTGTC 377						
QY	368 ATATTTGATGAGGTTTGTGAGTGGTGGAGCTTTTGTGCGGATGTTTCTAAGGTC 427						
Db	378 ATATTTGATGAGGTTTGTGAGTGGTGGAGCTTTTGTGCGGATGTTTCTAAGGTC 437						
QY	428 ATTTTATGAGCGGTGAAGCTGTCAAGCTTATTAAAGACGATTCCTGGTGTGTTGAGGCTT 487						
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Db	558 CTAAGATGATGCTAAGCTTAAGGCTACCGATT 591						
RESULT 3							
LOCUS	AY109374						
DEFINITION	Zea mays CL146_1 mRNA sequence.						
ACCESSION	AY109374						
VERSION	AY109374.1 GI:21213078						
KEYWORDS	HTC.						
SOURCE	Zea mays.						
ORGANISM	Zea mays						
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC						
AUTHORS	Hayney,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S., Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.						

791 AGTTAGATTCAAAATCTGACCCGTGGCTACTATCTCAGAGCTGCTAAAGATTGATCT 850
Db 1418 GCTCGACTTCAGTTCGAGCGGTGGCCAGCATCTCGAGCGCGCCAGAGATCTCGTGA 1477
Qy 851 ATAAATGCTCGAAGGAGCCCAAGAAACGATTTCTGCTCATGAAGCCTTGTGTCACC 910
Db 1478 GGAGGATGCTTCTCAGGAGCCGAGGAAGAGACTGACCGCTCAGGAAGTCTCAGGCATC 1537
Qy 911 CATGATTGTCGATGAACAAGCAGCAGCAGCAAGCCCTCTTGATCCAGCAGTCTTATCTC 970
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Qy 1091 ACAACAGCGGAACGATTTCTTTTGAAGAGCTCAAAAGCGGTTTGAAGAGTCTGATCTG 1150
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Qy 1151 AACTGATGAATCAGAAATCAAGTCTCTCATGATCGCGCTGATATCGACAACAGTGTGA 1210
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Qy 1211 CAATAGACTACGAGAAATCTTAGCAGCAACCTTACATAGAACAAAGATGGAGAGAGG 1270
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Qy 1271 AGATTCTGGTGGCTGATTTTCGAGCTTTGACAAAGACGGAAGCGTTATATCACCATCG 1330
Db 1898 ACCACCTGTTTCGGCGGCTCCAGTACTTCGACAGAGCGGACCGGNNNNNNNNNN 1957
Qy 1331 ATGAGCTTACGTCAGCTTGCACAGAGTTTGGTCTATGATACACTCTGACGACATGA 1390
Db 1958 NNN 2017
Qy 1391 TCAAGGAGATGATCTTGACAAAGCGGGAAGATCGATTCTCGGAGTTTACAGCAATGA 1450
Db 2018 TCGGGGAAGTCGACCAAGCAACAGCGGGGCGCATAGACTACACAGATTTCGTGGCGATGA 2077
Qy 1451 TGAGGAA 1457
Db 2078 TGAGGAA 2084

RESULT 4
LOCUS AY109401 2298 bp mRNA linear HTC 25-MAY-2002
DEFINITION Zea mays CL1577_1 mRNA sequence.
ACCESSION AY109401
VERSION AY109401.1 GI:21213112
KEYWORDS HTC.
SOURCE Zea mays.
ORGANISM Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PAC
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 2298)
Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S.,
Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.
Maize Mapping Project/DuPont Consensus Sequences for Design of
Overgo Probes
Unpublished (2002)
2 (bases 1 to 2298)
Coe, E.C.
Direct Submission
Submitted (25-APR-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 65211, USA
Location/Qualifiers

source 1. 2298
/organism="Zea mays"
/db_xref="MaizeDB:630430"
/db_xref="taxon:4577"
/clone="CL1577_1"
/clone_lib="Maize Mapping Project/DuPont Consensus
Library"
/notes="this sequence is part of a project of EST
assemblies resulting from the application of public
contigs to seed DuPont contigs; this resource was
assembled by DuPont as part of a collaboration for the
overgo addressing of BACs in conjunction with the Maize
Mapping Project"

BASE COUNT 544 a 464 c 597 g 524 t 169 others
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Best Local Similarity 61.8%; Pred. No. 9.9e-83;
Matches 817; Conservative 0; Mismatches 502; Indels 3; Gaps 1;

Qy 142 TACCTTCTGGGAAAAAGCTAGGCCAAGGCAATTTTGGAAACAACCTATCTCTGCACAGAG 201
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Qy 202 AAATCAACTCGCTTAATAGCCTTGCAAATCGATCCGGAAGCGAAGCTCGTGTGCGC 261
Db 726 GTTGCTCTGGAGGCGAGTACGCTTCAAGTCCATCTCCAAGCGCAAGCTCGCCAGAG 785
Qy 262 GAGGATTACGAGATGATGCGGTGAGATTCAGATCATCATCTCTCTGAGCATCCA 321
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Qy 322 AATGTTGTAGGATCAAAAGGCACTTATGAAGTTCGGTGTGTTGTTCAATTTGTTATGGAG 381
Db 846 AACATTGTCAGTTCCGGGAGCATACGAGCAAGAGCAATGTCCATGTGGTATGGAG 905
Qy 382 GTTTGTAAGTGTGAGCTTTTTCATCGGATTTCTTAAAGTCAATTTAGTGACCGT 441
Db 906 CTCTGCGCAGGTGGGAGCTCTTCAICGCACTATTGCAAGGGGCACTACACAGAGCGT 965
Qy 442 GAAGCTGTCAAGCTTTATTAAGACGATCTTGGTGTGTTGAGGCTTGTCAATCTCTCTGGT 501
Db 966 GCGGCTGCTACAATCTGCAGAGCAGTTGTGAATGTGTCAACATTTGCCACTTCATGGGT 1025
Qy 502 GTTATGATAGAGATCTCAAACTGAGATTTCTTGTGATGATCTCTTAAAGATGATGCT 561
Db 1026 GTGATGACCGTCACTTGAACCGGAGAACTTTCTGTCGACCAAGGAGGAAATGCA 1085
Qy 562 AAGCTTAAGGCTACCGATTTTGGTTTGTCTCTTCTATAAGCCAGGACAATATTTATAT 621
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Qy 682 GAAATAGATGTGGAGTCTGCTGTATCTCTTCAATTTTACTCAGCGGTGTTCTCTCC 741
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Db 1386 ACAGGAGATCCAAAGAAAGAGACTGACTTCAGCTCAAGTTCTTCAACATTCATGGCTCAGA 1445
Qy 922 GATCAACAGCACACCAAGCAAGCCCTTTGATCCAGAGCTTCTTATCTCGTCTAAAGCAG 981


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Db 1446 GAAGTGGAGTGCATCTGATGAAGCCTATCGACAGTCTGCTTTCTTAGAATGAAGCAG 1505
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QY 1222 GGAGAAATTCCTAGCAGCAACTTACACATGAACAAAGATGGAGAGAGAGATCTGGTG 1281
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QY 1282 GCTGCATTTTCGGATTGTGACAAAGACGAGCGGTTATATCAACATCGATGAGCTTCAG 1341
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QY 1342 TCAGTTCCACAGAGTTTGGTCTATGTGATAC---ACCTCGACGACATGATCAAGGAG 1398
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QY 1399 ATTGATCTTGACATGACGGGAAGATCGATTCTCGGAGTTTACAGCAATGATGAGGAA 1458
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QY 1459 GG 1460
Db 1986 GG 1987

RESULT 5
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LOCUS AV558412 Arabidopsis thaliana green siliques Columbia Arabidopsis
DEFINITION thaliana cDNA clone SQ098B02F 3', mRNA sequence.
ACCESSION AV558412
VERSION AV558412.1 GI:8729838
KEYWORDS EST.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
TITLE Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 507)
ASAMIZU, E., NAKAMURA, Y., SATO, S. and TABATA, S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation
of 12,028 non-redundant expressed sequence tags from normalized and
size-selected cDNA libraries
JOURNAL DNA Res. 7, 175-180 (2000)
MEDLINE 20363093
COMMENT Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.
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FEATURES
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Best Local Similarity 59.6%; Pred. No. 3.6e-82;
Matches 505; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 1301 ACAAGAGAGAGAGAGAGAGAGATTCACCATGATGAGTTCAGTCAGCTTCACAGAGTTG 1360
Db 447 ACAAGAGAGAGAGAGAGAGATTCACCATGATGAGTTCAGTCAGCTTCACAGAGTTG 388
QY 1361 GTCTATCTGATACACCTCTCGAGCAGATGATCAAGAGAGATTCATCTTGACAATGACGGGA 1420
Db 387 GTCTATCTGATACACCTCTCGAGCAGATGATCAAGAGAGATTCATCTTGACAATGACGGGA 328
QY 1421 AGATCGATTTCTCGAGATTTACAGCAATGATGAGGAAGAGATGGAGTTGGAGAGCA 1480
Db 327 AGATCGATTTCTCGAGATTTACAGCAATGATGAGGAAGAGATGGAGTTGGAGAGCA 268
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LOCUS BG647837 HOGA Medicago truncatula cDNA clone PHOGA-1855 5' end,
DEFINITION mRNA sequence.
ACCESSION BG647837
VERSION BG647837.1 GI:13782949
KEYWORDS EST.
SOURCE barrel medic.
ORGANISM Medicago truncatula
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
TITLE Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
1 (bases 1 to 835)
Hahn, M.G., Ojanen-Reuhs, T., Samac, D., Town, C.D., Van Aken, S.,
Uterback, T., Cho, J. and Fraser, C.M.
ESTs from roots of Medicago truncatula treated with
oligogalacturonides of DP 6-20
JOURNAL Unpublished (2001)
MEDLINE
COMMENT Contact: Michael G. Hahn
Complex Carbohydrate Research Center
University of Georgia
220 Riverbend Road, Athens, GA 30602-4712, USA
Tel: 706-542-4457
Fax: 706-542-4412
Email: hahn@ccrc.uga.edu

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QY 409 CGGATTGTTCTAAAGTGCAITTTAGTGAGCGGTGAAGCTGCTCAAGCTTATTAAAGACGATT 468
 Db 1375 CGCATCATAGCAAGGCGCCACTACACGAGCGNNNNNNNNNNNNNNNNNNNNNNNGATC 1316
 QY 469 CTTGTGTGTTGAGGCTTGTCATCTCTGGTGTATATGATAGATCTCAAAACCTGAG 528
 Db 1315 GTGCGCGTCGTCACAGCTGCCACTCATNNNNNTCTTCCATCGGATCTCAAGCCCGAG 1256
 QY 529 AATTCTCTGTTGATGCTCTAAAGATGATGCTAAAGCTTAAGGCTACCGATTTTGGTTTG 588
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 QY 589 TCTGTCTCTTAAGCCAGGACATATTTATATGACGTAGTCTGGAAGTCCGACTATGTT 648
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 Db 475 CACAGCGGATACATAACCGTAGATGATTTGGAAGAGCTTTGAGAGATGATATGGA 416
 QY 1366 TGTGATACACTTGGACGACATGNTCAGAGAGATGATGATGATGATGATGATGATGATG 1425
 Db 415 GATGACAAAACATAAAGAAATCATTTGCTGAGTATGATACAGATCATGATGGAAGAT 356
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 Db 355 AATTACAGAGGTTTGTGCGATGATGAGAA 324

RESULT 8
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 VERSION
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 ORGANISM
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 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 CONTACT: Cathy Ronning
 The Institute for Genomic Research
 For clone info: please contact Research Genetics, Libraries
 Division tel 1-800-711-6195, email cdna@resgen.com
 Seq primer: M13F-R.
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 BASE COUNT 242 a 146 c 191 g 235 t
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 Query Match 26.7%; Score 456.8; DB 12; Length 814;
 Best Local Similarity 73.3%; Pred No. 1.8e-75;
 Matches 597; Conservative 0; Mismatches 217; Indels 0; Gaps 0;
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 Db 1 GAGAAAAGCTGCACAATTGATGAAAACCTATTGTCAAAGTTGTGGAGGCTTGTCTCTCT 60
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 QY 618 ATATGACGTAGTTGGAAGTCCGCTACTATGTTGCACGAGGCTGCTAAAGAAATTTTGG 677
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Db 361 CTTTGAATCAGAACTTGGCCCTCAGATTTCTGATAGTGCAGAAAGATTTGGTAAAGAGAT 420
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Db 421 GGTACACAGGATCCTAGAGCAGCATTAACCGCGCATCAAGTTCTATGTCTATCTTGGAT 480
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Qy 1158 GGAATCAGAAATCAAGTCTCTCATGATGCGGCTGATATCAGACACAGTGTACATAGA 1217
Db 721 AGAGTCCGAAATCAAGGCTTGTATGAGCGGCTGACTTTGACAAACAGCGCACTATCGAC 780
Qy 1218 CTACGAGAAATTCCTAGCAGCAACCTTACACATG 1251
Db 781 TATGGTGATTCATCGCTGCAACATTGCAATTG 814

RESULT 9
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LOCUS
DEFINITION
T8A20TFB TAMU Arabidopsis thaliana genomic clone T8A20, DNA
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B28263
B28263.1 GI:2514229
GSS.
SOURCE
thale cress.
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 493)
REFERENCE
Rounsley,S.D., Kelley,J.M., Field,C.E., Craven,M.B., Adams,M.D. and
Venter,J.C.
Use of a BAC End Sequence Database To Identify Minimal Overlaps for
Arabidopsis Genomic Sequencing
Unpublished (1997)
Other GSSs: T8A20TR
Contact: Steve Rounsley
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: rounsley@tigr.org
Seq primer: M13-21
Class: BAC ends
High quality sequence stop: 493.
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/db_xref="taxon:3702"
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BASE COUNT 126 a 110 c 95 g 162 t

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ORIGIN

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Query Match 25.1%; Score 439; DB 17; Length 493;
Best Local Similarity 100.0%; Pred. No. 2.4e-70; Mismatches 0; Indels 0; Gaps 0;
Matches 439; Conservative 0;
Qy 18 TTCTTTCTTCAAAATCGAGATCGAAGAAGAACCAACCAAAAAACCAAAAAATGGAGACGAA 77
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Qy 438 GCGTGAAGCTCTCAAGCTT 456
Db 20 GCGTGAAGCTCTCAAGCTT 2

RESULT 10
B11596/c
LOCUS
DEFINITION
B11596
B11596.1 GI:2092717
GSS.
SOURCE
thale cress.
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 1087)
REFERENCE
Feng,J., Dewar,K., Buehler,E., Kim,C., Li,Y., Shinn,P., Sun,H. and
Ecker,J.
BAC End Sequences at ATGC
Unpublished (1997)
Contact: Ecker J.
Arabidopsis Thaliana Genome Center
University of Pennsylvania
Dept. of Biology, University of Pennsylvania, Philadelphia, PA
19104
Tel: 215-898-9384
Fax: 215-898-8780
Email: jecker@atgenome.bio.upenn.edu
Seq primer: T7
Class: BAC ends
High quality sequence start: 93
High quality sequence stop: 873.
Location/Qualifiers
1. .1087
/organism="Arabidopsis thaliana"
/strain="Columbia"

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FEATURES

source

3

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D_b 271 GAGATTCAGATAATGCACCATTTGTCTGAAATCCAAATGTTGTGAGGATCCATGGAACT 330

346 TATGAGATTCCGTTGTTTTCATATTTATGAGGTTTGTGAAAGTGTGAGCTTTT 405
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 331 TACGAGGATTGGTTTCTGTTCAATTTGTTATGAGCTTTGTGAAGTGGGAATGTT 390
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 406 GATCGATTGTTCTTAAGGTCATTTTAGTCAGCGTGAAGCTGTCAGACTTATAGACG 465
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 825 CTCA 828
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 810 TTCA 813

RESULT 14
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 DEFINITION mRNA sequence.
 ACCESSION B1178776
 VERSION B1178776.1 GI:14644587
 KEYWORDS EST.
 SOURCE potato.
 ORGANISM Solanum tuberosum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridaceae; euasterids I; Solanales; Solanaceae; Solanum.
 1 (bases 1 to 686)
 van der Hoeven,R., Bezzerides,J., Bachem,C., Visser,R., Cho,J.,
 Chlemingo,A., Bougri,O., Buell,C.R., Ronning,C., Tanksley,S. and
 Baker,B.
 Generation of ESTs from in vitro grown microtubers
 Unpublished (2001)
 Contact: Cathy Ronning
 The Institute for Genomic Research
 For clone info: please contact Research Genetics, Libraries
 Division tel 1-800-711-6195, email cdna@resgen.com
 Seq primer: M13P-R.
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RESULT 15

/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
 XhoI; Tissue supplied by Christian Bachem and Richard
 Visser (Department of Plant Breeding, Wageningen
 University, The Netherlands). The cSTA libraries will
 attempt to capture the induction and initiation/initial
 growth of the tuber in an in vitro system as described in
 Bachem et al. (Plant Journal, 1996). Small microtubers
 develop from axillary buds attached to stem explants when
 placed on a high sucrose medium (10%). Visible
 morphological changes occur synchronously at day five in
 the axillary buds. The first library, cSTA (1-20) consists
 of axillary buds harvested on days 1-3. This targets
 those genes involved in induction of the microtubers. The
 following libraries, cSTA (21-40) and cSTA (41-60)
 capture genes involved in tuber initiation and outgrowth.
 This library is noted as P3 in Tanksley lab notebooks."

BASE COUNT 198 a 122 c 162 g 204 t
 ORIGIN
 Query Match 23.0%; Score 401.8; DB 13; Length 686;
 Best Local Similarity 74.2%; Pred. No. 1.3e-63;
 Matches 508; Conservative 0; Mismatches 177; Indels 0; Gaps 0;
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 QY 622 GACGTAGTTGGAAGTCGCTACTATGTTGCACAGAGGTGCTAAAGAAATCTTAGACCT 681
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 Db 481 GATGACTCAATGACCCCTGATTAACCTTCTTGTTCAGTTCTTTTACCCCTCAAGCAA 540
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 Db 541 TTCTCAGCAATGAACAAACTAAAGAAATGGCTTTTGGCTGTGTGTTGCCAGAGAGCTATCA 600
 QY 1042 GAGGAGAAATGGAGGTCTGAAGGAATTTGTCAGATGATAGACAGACAGACAGCGGA 1101
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B0865474
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 DEFINITION QG5A16.1 Yg.abl QG ABCDI lettuce salinas Lactuca sativa cDNA clone
 QG5A16.1 mRNA sequence.
 ACCESSION B0865474
 VERSION B0865474.1 GI:22250939
 KEYWORDS EST.
 SOURCE Lactuca sativa.
 ORGANISM Lactuca sativa.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
 Lactuca.
 1 (bases 1 to 751)
 Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Riesberg, L.,
 Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J., Ellison,
 P., Kolman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z.,
 Church, S., Jackson, L., and Bradford, K.
 Lettuce and Sunflower ESTs from the Compositae Genome Project
 http://comgenomics.ucdavis.edu/
 Unpublished (2002)
 Contact: Alexander Kozik [R.W.Michelmore]
 Department of Vegetable Crops, R.W.Michelmore Lab
 University of California at Davis (UCD)
 Asmudson Hall, UCD, Davis, CA 95616, USA
 Tel: 1-(530)-742-1742
 Fax: 1-(530)-752-9659
 Email: akozik@ucdavis.edu [michelmore@vegmil.ucdavis.edu]
 belongs to contig QG_CA_Contig3691, see http://cgdb.ucdavis.edu/
 for details.
 Plate: QGCS row: A column: 16.

FEATURES
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 /lab_host="E.coli"
 /note="Vector: pBRCDNAS1AB; The library was constructed
 from 10 different sources of RNA from a single genotype.
 Separate cDNAs were generated using primers that
 incorporated unique 5' and 3' tags to distinguish each
 source of RNA. cDNAs were then pooled, size-fractionated,
 directionally cloned into a custom medium-copy vector and
 transformations made with four size classes to minimize
 size bias. Details of each source of RNA and library
 construction can be obtained at http://cgdb.ucdavis.edu/
 TAG LIB=QG ABCDI lettuce salinas
 TAG TISSUE=chemical induction
 TAG_SEQ=GTGAGCCGGG"
 BASE COUNT 218 a 117 c 180 g 236 t

Query Match 22.3%; Score 388.8; DB 14; Length 751;
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 QY 347 ATGAAGATTCGGTGTGTTGTTATGTTATGAGGTTTGTGAAGTGTGAGCTTTTGG 406
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 QY 407 ATCGATTGTTTAAAGTCAATTTATGAGCGGTGAAGCTGTCAGCTTATTAAGACGA 466
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Search completed: February 13, 2003, 19:51:19
 Job time : 2599 secs

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 QY 1007 AAATGGCATTAACGGGTAAATGCTCGAGAG 1034
 Db 720 AAATGGCTTTGAGGTTATAGCTGAGAG 747